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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 16, 2004, 15:21:38; Search time 17 Seconds (without alignments) 891.319 Million cell updates/sec Run on:

US-09-936-845A-15 1545 1 MELABFWNDLNTFTIYGPNH.....PFVKAYIIKSSKKSKSVKNE 291 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMENTES

		Description	_		Q9hb03 homo sapien		O9eqc4 mus musculu	P40319 saccharomyc	Q95k73 macaca fasc	Son	Q9jlj5 mus musculu		P39540 saccharomyc	P25358 saccharomyc	09jlj4 mus musculu					Q9vhe6 drosophila		homo						caenc	pomo	homo	Wiggl	_	3 rati	2723	P39129 bacillus su
SUMMARIES	į	ar .	YLF4_CAEEL	YYS3_CAEBL	ELO3 HUMAN	ELO3 MOUSE	ELO4_MOUSE	ELO3 YEAST	ELO4 MACFA		ELO1 MOUSE			ELO2 YEAST	ELO2 MOUSE	ELO2_HUMAN	YE21_ARCFU	YKQ5_YEAST	TLCA_RICPR	O85F DROME	NORE PSEST	E124 HUMAN	IP3T HUMAN	NAHB_ONCMY	ALG8_HUMAN	Y771_ARCFU	O6N2_HUMAN	ALG6_CAESL	CTR1 HUMAN	FZD9 HUMAN		NORE PSEAE	GAC2_RAT	GAC2_MOUSE	LPLC_BACSU
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	% Query	Length	291	435	270	271	312	345	314	314	279	279	310	347	292	296	880	919	498	392	473	359	2671	759	526	289	317	503	629	591	873	466	9	r	295
	Query	Match	00.	36.5		31.0			16.9		'n.	15.	14.	14.2	14.	13.	9	9	6.3	6.2					•	•	•		•	υ. 9	•	•	•	•	5. B
	į	Score	54		ð	Γ~		w	261	LO.	239.5	239	220.5	220	219	214	102	99.5	97.5	Ġ	96	95	9	93.5	92			91.5	•	1 6	6 6	90.5	06	g,	89.5
	Result	2	m	63	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P18794 streptococc	P21548 gallus gali	Q9jlg4 mus musculu	P51533 saccharomyc	052535 klebsiella	P98059 rhodobacter	Q61070 mus musculu	P35855 lactobacill	P18507 homo sapien	P34322 caenorhabdi	Q9ze15 rickettsia	Q92670 zymomonas m
AMID STRPN	GAC2_CHICK	P2L2 MOUSE	PDRA_YEAST	CAH KLEPN	COXI_RHOCA	RI24 MOUSE	DLTB_LACRH	GAC2_HUMAN	YKTA_CAEEL	Y147 RICPR	GNTP_ZYMMO
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308	474	621	1564	246	532	358	405	467	290	236	451
ري 9.	ю. В	ю. Ф	ъ. В	5.7	5.7	5.7	5.7	5.7	5.6	5,6	5.6
89.5	6 0	80	68	88.5	88.5	88	88	88	87	86	86
3.4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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103 FSIDPLRSLYAEG--FYKTLCYSCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIF 160
                                                        65 SRVITPESSLQNAIKNRNKKSLNSSQMFQIMEKYKPPQLDTPLFVWNSPLAIFSILGFLR 124
OKF--MENRKPFTLKYPLILWNGALAAFSIIATLR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 35-270 FROM N.A.
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                279 IKSSK 283
                                                                                                                                                                                                       302 KKINNR 306
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                  LYFILIKVIQKFMENRKPFTLKYPLILMWGALAAFSIIATLRFSIDPLRSLYABGFYKTL 120
                                                                              LYFILIKVIQKPMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL 120
                                                                                                                180
                                                                                                                             CYSCNPTDVAAFWSFAFASKIVBLGDIMFILLRKRPLIFLHYYHHAAVLIYTVHSGAEH 180
                                                                                                                                                                                  240
                                                                                                                                                            TAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKV 240
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                                     1 MELAEFWNDLNTFTIYGFNHTDMTTKYKYSYHFPGEQVADPQYWTLLFQKYWYHSITISV
                                                                                                                                                                         TAAGREYILMNYEAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKV
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                        1 MELAEPWNDLNTFTIYGPNHTDMTTKYKYSYHFPGGQVADPQYWTILFQKYWYHSITISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWTTKY----KYSYHEPGEQVADPQYWTILFQKYWYHSITISVLYFILI----KVI----
  Gaps
                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Caps
                                                                                                                                                                                                       241 KTEYKLPCQQSVANLYLAFVIYVTFALLPIQFFVKAYIIKSSKKSKSVKNE 291
                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
STRAIN-Bristol N2;
Du Z., Gattung S.;
Submitted (NOV-1995) to the EWBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the ELO family.
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                                                                                                                                                                                                                   KTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSKVRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Indels
  0; Indels
                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
43-FEB-203 (Rel. 41, Last annotation update)
Hypothetical 51.5 kDa protein D2024.3 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
F7940A74A1969914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.5%; Score 564; DB 1;
42.0%; Pred. No. 1.4e-39;
tive 45; Mismatches 86;
                                                                                                                                                                                                                                                                                      435 AA.
  Mismatches
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POTENTIAL.
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InterPro; IPR002076; GNS1_SUR4.
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PROSITE; PS01188; ELO; 1.
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  291; Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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239 2
278 2
435 AA;
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SEQUENCE
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220
                                                   221 TVQTTQMLAGVGITWMVYKVKT--EYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse genomes..;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in a membrane event related to cellular proliferation in brown adipose tissue. Could be implicated in synthesis of very long chain fatty acids and sphingolipids. May catalyze one or both of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl CoA derivative (By similarity)
161 LHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Elongation of very long chain fatty acids protein 3 (Cold inducible glycoprotein of 30 kba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Semina B.V., Murray J.C.; "The CIG30/PITX3/GBF1 gene configuration is conserved between human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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involved in the recruitment of brown adipose tissue.";
                                                            SECUENCE FROM N.A.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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TRANSMEM 3
TRANSMEM 6
                                                                                                                                                                                                                                                          TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>:</u>:
    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outertation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GTVLITGGLKQTVCFINFIDNSTVKFWS#VFLLSKVIELGDTAFIILRKRPLIFIHWYHH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKNVSMTVTTVQTTQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STVLVYTSFGYRAKVPAGGWFVTWNFGVFAIKYTYTTLKAANVKPPROLITSLQILQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 MFVGAIVSILTYIWRQDQ--GCHTTMEHLFWSFILYMTYFILFAHFFCQTYIRFKVKAKT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 FEEYWATSFPIALIYLVLIAVGONYMKERKGFNLOGPLILWSFCLAIFSILGAVRMWGIM 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Elongation of very long chain fatty acids protein 3 (Cold inducible glycoprotein of 30 kDa) (CIN-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Cig30, a mouse member of a novel membrane protein gene family, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                           Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum. TRANSMEM 29 49 POTENTIAL. TRANSMEM 66 86 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE-Brown adipose tissue;
MEDLINE-98058971; PubMed-9395518;
Tvrdik P., Asadi A., Kozak L.P., Nedergaard J., Cannon B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
OCGCBF1E7B5DE8B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 492; DB 1;
Pred. No. 7.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches
                      SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                        Genew; HGNC:18047; ELOVL3.
InterPro; 1FR0080705; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                 EMBL; BC034344; AAH34344.1; -.
EMBL; AF292387; AAG17875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31500 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%;
    reticulum (Potential).
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                                                                                                                                                                                                                                                                                                                                                            49
86
186
218
255
268
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RECONTINE-22388257; PubMed-12477932;

RA STRUBE-1108-22388257; PubMed-12477932;

RA Klausner R.D., Collins F.S., Magner L., Sheamen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschehol L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rabla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Nitlaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rheby J., Helton E., Ketteman M., Mardan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Rad Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT Thurnon and initial analysis of more than 15,000 full-length

RT Thurnon and initial analysis of more than 15,000 full-length

RT Thurnon and initial analysis of more than 15,000 full-length

RT Thurnon Nay be involved in a membrane event related to cellular

C. PUNCTION: May be involved in a membrane event related to cellular

C. PUNCTION: May be involved in a membrane event related to cellular

C. Catalyze one or both of the reduction of trans-2-enoyl CoA to the saturated

C. Catalyze one or both of the reduction of trans-2-enoyl CoA to the saturated

C. Hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated

C. Hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institute. There are no restrictions on its modified and this statement is not way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- INDUCTION: Elevated in brown adipose tissue in conditions of brown far recruitment, namely cold stress, perinatal development and after diet-induced thermogenesis. A symergiatic action of both catecholamines and glucocorticoids is required for the induction.
-:- SIMILARITY: Belongs to the BLO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Readily detected in brown adipose tissue and liver. Weak expression in Kidney, white adipose tissue, heart and skin. Not detected in lung, testis, muscle, spleen, brain, thymus and innestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                  STRAIN=129/SvJ;

MEDLINE=94030815, PubMed=10473596;

MEDLINEE, 94030815, V. Kozak L.P., Nuglozeh E., Parente F.,

Nedergaard J., Jacobsson A.;

Cig30 and Pitx3 genes are arranged in a partially overlapping

"Cig30 and Pitx3 genes are arranged in complementary transcripts.";

J. Biol. Chem. 274:26387-26392(1999).
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Biol. Chem. 272;31738-31746(1997).
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InterPro; IPR002076; GNS1_SUR4.
Pfam; PP01151; ELO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U97107; AAC06127.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01188; ELO; 1. Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reticulum (Potential)
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or send an email to license@isb-sib.ch)
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312 AA;
                                                                                                                                                                                                                         Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxED=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAST
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P40319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLO3_YEAST
                                                                                                                                                     SITE
                                                                                                                                                                                                                                   Matches
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                                                                                                                   4,
                                                                                                                                                                                                                                    AVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLЭKWVSMTVTTVQTTQM 227
                                                                                                                                        QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                                                                                                                               109 RSLYABGGTYKTLCYSCNPTD-VAAFWSFARALSKIVELGDTWFIILRKKRPLIFLHYYHHA 167
                                                                                                                                                                                                   TVLLFTSFCYKNKVPSGGWFWTWNPGVHSVMYTYTWKAARLAKFPNLLPWVITSLQILQM 211
                                                                                                                                                                                                                                                                                    LAGV--GITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSK-K 284
                                                                                                                                                                5
                                                                                                                                                       EEYWVSSFLIVVVYLLLIVVGQTYMRTRKSFSLQRPLIHWSPFLAIFSILGTLRWWKFMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum (Potential).
TISSUE SPECIFICITY: Expressed in the adult retina, exclusively in
photoreceptor cells.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CSTBE,/6; TISSUE=Testis;
MEDLINE=20578755; PubMed=11138005;
MEDLINE=20578755; PubMed=11138005;
Metzker M.L., Allikmets R., Zack D.J., Kakuk L.B., Lagali P.S., Wong P.W., McDonald I.M., Sieving P.A., Figueroa D.J., Austin C.P., Gould R.J., Ayyagari R., Petrukhin K.;
M.A. S.-bp deletion in ELOVIA is associated with two related forms of autosomal dominant macular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Involved in the biosynthesis of very long chain fatty acids. Seems to represent a photoreceptor-specific component of the fatty acid elongation system residing on the endoplasmic
           POTENTIAL.
POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCRLIULAR LOCATION: Integral membrane protein. Endoplasmic
                                                        N-LINKED (GLCNAC. . .) (POTENTIAL) 
F7CA96199BE89401 CRC64;
                                                                                                                   8,
                                                                                           Length 271;
                                                                                                                   87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FSB-2003 (Rel. 41, Created)
8-FSB-2003 (Rel. 41, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Elongation of very long chain fatty acids protein
                                                                                           Score 479; DB 1;
Pred. No. 9.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                   47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                 312
                                              (POTENTIAL)
 POTENTIAL
                                                          6 N
32060 MW;
                                                                                           31.0%;
                                                                                                        41.6%;
                                                                                                                   101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
 187
219
256
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                     271 AA;
                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         270
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                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
           TRANSMEM
TRANSMEM
SITE
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                                                                                                                                                                                                                                                                                                           212
                                                         CARBOHYD
                                                                                            Query Match
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                                                                     SEQUENCE
 IRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 FYILMNYFAHSLMYTYYTVSAMGYRLPK--WVSMTVTTVQTTQMLAGVGITWMVYKVKTB 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 RLVLIIYNFGMVLLNLFI-----FRELFMGSYNAGYSYIÖQSVDYSNDVNEVRIAAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AFWSFAFALSKIVELGDTMFIILRKR--PLIFLHYYHHAAVLIYTV-HSGAEHTAAGR-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVBEYRWIWIIADKRVAD---WP-LMQSPW-PIISISTLYLLFVWLGPKWMKDREPFQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 DMITKYKYSYHPPGBQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P40319;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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MEDLINE=96220455; PubMed=8649379;
MEDLINE=96220455; PubMed=8649379;
Silve S., Leplacois P., Josse A., Dupuy P.-H., Lanau C., Kaghad Silve S., Leplacois P., Josse A., Taton M., Le Fur G., Caput D., Dhers C., Picard C., Rahler A., Taton M., Le Fur G., Caput D., Dhers C., Picard C., Rahler A., Taton M., Le Fur G., Caput D., Dhers C., Picard C., Rahler A., Taton M., Le Fur G., Caput D., Dhers C., Picard C., Rahler A., Taton M., Le Fur G., Caput D., Le Fur G., Caput D., Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . (POTENTIAL). CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CPFP-----KWMHWALIAYAISFIFLFINFYTRITNEPKQSKTGKTATN 284
                                                                                                                                                                                                                                              Transmembrane; Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara P., Loison G., "The immunosuppressant SR 31747 blocks cell proliferation by inhibiting a steroid isomerase in Saccharomyces cerevisiae.", Mol. Cell. Biol. 16:2719-2727(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 YKLPCQOSVANLYLAFVIY-VTFAILFIOFFVKAY-IIKSSKKSKSVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 KYPLILMMGALAAPSIIATLRFSIDPLRSLYABGFYKTLCYSCNPTD-
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ELO3 OR SUR4 OR SREI OR APAI OR VBMI OR VLR372W OR L8 Saccharowyces cerevisiae (Baker's yeast).

ElVatryota, Fungi, Ascomycota, Saccharomycotina, Sacch Saccharomycetales, Saccharomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 263.5; DB 1; 28.7%; Pred. No. 7.8e-15; ive 53; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC.
B04CD48024772132 (
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Thesis (1994), University of Bordeaux II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
EMBL: AF277093; AAG47667.1; -. MGD: MGI:1933331; Elov14.
InterPro; IPR002076; GNS1_SUR4.
Ffan: PF01151; ELO; 1.
PROSITE: PS01188; ELO; 1.
PROSITE: PS01188; ELO; 1.
TRANSMEM 42 62 POTT
TRANSMEM 78 98 POTT
TRANSMEM 165 185 POTT
TRANSMEM 188 208 POTT
TRANSMEM 246 266 POTT
TRANSMEM 246 266 POTT
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36520 MW;
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STRAIN=ATCC 44827 / SKQ2N;
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                                                                                                                                                                                                                                                                                                      62
98
185
208
266
310
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STATHS=S2866 / AB972;
MEDLINE=97313267; PubMed=9169871;
Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Johnston M., Hillier L., Riles L., Dubois B., Duesterchoeft A., Brian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Ketter P., Heuss-Neitzel D., Hilbert H., Higer P., Kleine K., Koetter P., Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Ameller -Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Scholler P., Schwager C., Schwarz S., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann P.K., Zollner A., Hani J., Hoheisel J.D., I. The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstands. The between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elongation in the trafficking of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FINCTION: Affects plasma membrane H+-ATPase activity. May act on a glucose-signaling pathway that controls the expression of several glucose-signaling pathway that controls the expression of several glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose such as PMA1, HXT3 AND SNF3. Could be also a component of the membrane bound fatty acid elongation systems that produce the 26-carbon very long chain fatty acids that are precursors for ceramide and sphingolipids. Is essential for the conversion of 24-carbon fatty acids to 26 carbon species.

SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                      Garcia-Arranz M., Maldonado A.M., Mazon M.J., Portillo F.;
"Transcriptional control of yeast plasma membrane H(+)-ATPase by
glucose. Cloning and characterization of a new gene involved in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97362220; PubMed=9211877;
Oh C.-S., TOKE D.A., Mandala S., Martin C.E.;
"ELO2 and ELO3, homologues of the Saccharomyces cerevisiae ELO1 gene,
function in fatty acid elongation and are required for sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0005783, C:endoplasmic reticulum, IDA.
GO; GO:000922; F:fatty acid elongase activity, IMP.
GO; GO:0030497; P:fatty acid elongasion; IMP.
GO; GO:003048; P:post-Golgi transport; IGI.
GO; GO:0031189; P:sphingolipid biosynthesis; IMP.
INTERPRO, IPRO2076; GNSI_SUR4.
PROSITE; PS01189; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99054745; PubMed=9832547;
David D., Sundarababu S., Gerst J.E.,
"Involvement of long chain fatty acid
secretory vesicles in yeast.";
J. Cell Biol. 143:1167-1182(1998).
                                                                                            regulation.";
J. Biol. Chem. 269:18076-18082(1994)
  MEDLINE=94299524; PubMed=8027068;
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EMBL, X8326; CAA55129.1; --
EMBL, U19103; AAB67563.1; --
EMBL, AF011409; AAC28398.1; --
EMBL, A8517; S48517; GermOnline; 142436; --
SGD; S0004364; SUR4.
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107
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                                                                                                                                                                                                                                                                                                   166 VELIDTVFLVLRRKKILFIHTYHHGATALLCYTQLIG--RTSVEWVVILLNIGVHVIMYW
                                                                                                                                                                                                                                                                                   143 VELGDIMFIILRKRPLIFLHYYHH--AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYT
                                                                                                                                                                                                                                                                                                                                                 TISSUB-Temporal cortex;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
*Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                     85 LILWNGALAAPSIIATLRPSIDPLRSLYAEGPYKTLC--YSCNPTDVAAFWSFAPALSKI
                                                                                                                                                                                                                                                                                                                                  YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBY------KLPCQ
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TISSUE SPECIFICITY: Expressed mainly in retina. Also expressed in
                                                                                                                                                            34; Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=22691545; PubMed=12806887;
Umeda S., Ayyagari R., Suzuki M.T., Ono F., Iwata F., Fujiki K.,
Kanai A., Takada Y., Yoshikawa Y., Tanaka Y., Iwata T.;
"Molecular cloning of ELCVU4 gene from cynomolgus monkey (Macaca fascicularis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                  Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                  250 QSVANLYLAFVIYVTPAILFIQFFVKAYIIKSSKK--SKSVKNE 291
                                                                                                                                                           53; Mismatches 115; Indels
                                                                                              I -> FY (IN RBF, 3).
1303A9ACS4BFFCCS CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last amnotation update)
Elongation of very long chain fatty acids 4 protein.
                                                                       E -> D (IN REF. 3).
W -> R (IN REF. 3).
                                                                                                                                   17.0%; Score 262; DB 1; 28.9%; Pred. No. 1.2e-14;
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126
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208
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345 AA;
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les 82; Conserv
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TISSUE=Brain;

X MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., RA Aleuschul S.F., Feingold E.A., Grouse L.H., Shemen C.M., Schuler G.D., Aleuschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Aleusch C.L., Marusina R., Parmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L., Stapleton M.J., Ugdin T.B., Proshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Ugdin T.B., Proshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Petchiyuki S., Carninci P., Prange C., RA Richards S., Morley W.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rallskey J., Helton B., Ketterman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rallska U., Shailwa D.E., Retranded Y.S.N., Krzywinski M.I., Skaiska U., Sanlus D.E., Rallsker G.D., Marra M.A., Marra M.A., Schein J.E., Warra M.A., Marra M.A., Rallsker G.D., Shein J.E., Shein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Pujimori Y., Komiyama M., Sugiyama T., Itite R., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Rawai-Ho Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Mareuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Sugiyama M., Marsawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masub Numan cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-22480060; PubMed=1259226;
Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
Rivolta C., Ayyagari R., Sieving P.A., Berson E.L., Dryja T.P.;
Mol. Vision 9:49-51(2003).
Inchinitis pigmentosa and Leber congenital amaurosis.";
Mol. Vision 9:49-51(2003).
Inchinitis Involved in the biosynthesis of very long chain fatty acids. Seems to represent a photoreceptor-specific component of acids. Seems to represent a photoreceptor-specific component of the fatty acid elongation system residing on the endoplasmic reticulum. May be implicated in docosahexaenoic acid (DHA)
biosynthesis, which requires dieterary consumption of the essential alpha-linolenic acid and a subsequent series of three elongation steps.
In SUPERLULURA LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                 MEDLINE-21464738; PubMed-11581213;
Redards A.O., Donoso L.A., Ritter R. III;
Rayards A.O., Donoso L.A., Ritter R. III;
"A movel gene for autosomal dominant Stargardt-like macular dystrophy
with homology to the SUMA protein family.";
Invest. Ophthalmol. Vis. Sci. 42:2652-2663(2001).
               Zhang K., Kniazeva M., Han M., Li W., Yu Z., Yang Z., Li Y., Metzker M.L., Allikmets R., Zack D.J., Kakuk L.E., Lagali P.S., Wong P.W., McDonald I.M., Sieving P.A., Figueroa D.J., Austin C.P., Gould R.J., Ayagari R., Petrukhin K., Ab S-bp deletion in ELOVIA is associated with two related forms of autosomal dominant macular dystrophy.";
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MEDLINE=20578755; PubMed=11138005;
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                                                                                                                                                                                                Nat. Genet. 27:89-93(2001).
                                                                                                                                                                                                                                                        SEQUENCE PROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGF---YKTLC----YSCNPTDV----A 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AFWSFAFALSKIVELGDTMFILLRKR--PLIFLHYYHHAAVLIYTV-HSGAEHTAAGR-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
560FE00C91D96766 CRC64;
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Fatty acid biosynthesis; Transmembrane, Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CPFP----KWMGHWALIAYAISPIPLFLNFYIRTY--KEPKKDKTGK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 YKLPCQQSVANLYLAFVIY-VTPAILFIQFFVKAYIIKSSKKSKSVK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.9%; Score 261; DB 1; Length 314; 30.3%; Pred. No. 1.3e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Mismatches
                                  SIMILARITY: Belongs to the BLO family.
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                             EMBL; AF461182; AA015594.1; ---
EMBL; AF461187; AA015601.1; ---
EMBL; AF461183; AA015601.1; JOINED.
EMBL; AF461184; AA015601.1; JOINED.
EMBL; AF461185; AA015601.1; JOINED.
EMBL; AF461186; AA015601.1; JOINED.
EMBL; AF061186; AA015601.1; JOINED.
EMBL; AB063100; EMB60806.1; --
INTERPRO; IPR002076; GNS1_SUR4.
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reticulum (Potential). TISSUE SPECIFICITY: Expressed in the retina and at much lower

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SEQUENCE FROM N.A., AND VARIANT VAL-299 IISSUE-Retina;

HUMAN

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NCBI_TaxID=10090;
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level in the brain.

DISBABS: Defects in ELOVL4 are the cause of Stargardt disease 3 (STGD3) [MIM:500110]. STGD3 is an autosomal dominant form of macular degeneration characterized by decreased visual acuity, macular atrophy, and extensive fundus flocks.

DISBASE: Defects in ELOVL4 are a cause of autosomal dominant Stargardt-like macular dystrophy (ADMD) [MIM:500110].

SIMILARITY: Belongs to the ELOVL4 gene;
DATABASE: NAME-MUtations of the ELOVL4 gene;
NOTE-Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/elovlmut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0008020; F:G-protein coupled photoreceptor activity; NAS. GO:0006633; P:fatty acid biosynthesis; NAS. InterPro; IPR002076; GNS1_SUR4.
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Q -> R (IN REF. 4).
B2BBCE54D868E96E CRC64;
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FFIG=VAR_017043.
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Pfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
Fatty acid biosynthesis; Transmembrane; Fatty acid biosynthesis; Transmembrane; Folymorphism; Stargardt disease; Vision.
Polymorphism; Stargardt disease; Vision.
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EMBL, AF279649; AAG47669.1; --
EMBL, AF279650; AAG47669.1; JOINED.
EMBL, AF279651; AAG47669.1; JOINED.
EMBL, AF279652; AAG47669.1; JOINED.
EMBL, AF279653; AAG47669.1; JOINED.
EMBL, AF277034; AAG47669.1; --
EMBL, AV037298; AAK66839.1; --
EMBL, AV032876; CAC19496.1; --
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314 AA;
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MIM; 600110;
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246 FRED 2010 RE1 41, THAT SECRET STANDARY 2010 FREDCOSONARY 200

247 FRED 2010 RE1 41, THAT SECRET STANDARY 2010 FROM 2010 FREDCOSONARY 2010 FRED
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens (Human)

NCBI_TaxID=9606;

OSBWGO; OSNVD9; OSY396; 28-FEB-2003 (Rel. 41, Created) 10-CCT-2003 (Rel. 42, Last sequence update) Blongation of very long chain fatty acids protein 1 (CGI-88) ELOVU, OR SSC1.

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SEQUENCE FROM N.A. MEDLINE=20272150; PubMed=10810093; Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.; Lai C.-H., Chou C.-Y., Ch'ang rese evolutionarily conserved in Caenorhabditis elegans by comparative proteomics."; Genome Res. 10:703-713(2000).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 DIMPIILRKR--PLIFLHYYHHAAVLIYTVHSGAEHT--AAGRFYILMNYFAHSLMYTYY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 TVSAMGYRLP----KGVSMTVTTVQTTQ-MLAGVGITWMVYKVKTEYKLPCQQSVANLY 256
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                                                                                                                                                                                                                              TISSUE SPECIFICITY: Expressed in a broad variety of tissues. Highly expressed in scomach, lung, kidney, skin and intentine. Moderately expressed in white adipose tissue, liver, spleen, brain, brown adipose tissue, heart and muscle. Weakly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 DIVIFILRKKDGQVIFLHVFH-SVLPMSWWWGIXIAPGGMGSFHAMINSSVHVVMYLYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 IIATLRFSIDPLRSLYAEGFYKTLCYSCNPTD-----VAAFWSFAFALSKIVELG
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
ENDOPLASMIC RETICULUM RETRIBVAL MOTIF
                                                                Nature 409:685-690(2001).

-!- FUNCTION: Could be implicated in tissue-specific synthesis of long chain fatty acids and sphingolipids. May catalyze one or be the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl COA to beta-hydroxyacyl COA or reduction of trans-2-enoyl COA to the saturated acyl COA
                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                            derivative.
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
TRANSMEM 23 43 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the ELO family.
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InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
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nes 78; Conserv
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Isogai T., Ote T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsurawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project."; Sasaki N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derivative (By similarity).
-:- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic retirolum (Potential).
-:- SIMILARITY: Belongs to the ELO family.
-:- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF151846; AAD34083.1; ALT_FRAMB.
EMBL; AK001653; BAA91813.1; -.
EMBL; BC000618; AAH00618.1; -.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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RESULT 10 ELO1_HUMAN

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                                                                                                                                                                                                                                                                                                              DTMFIILRKR--PLIFLHYYHHAAVLIYTVHSGAEHT--AAGRFYILMNYFAHSLMTTYY 202
                                                                                                                                                                                                                                                                                                                                  182
                                                                                                                                                                                                                                                                                                                                                          203 TVSAMGYRLP----KWVSMTVTTVQTTQ-MLAGVGITWMVYKVKTBYKLPCQQSVANLY 256
                                                                                                                                                                                                                                                                                                                                                                         183 GLSAPG----PVAQPYLWWKKHWTAIQLIQFVLVSLHISQYYFMSSCNYQYP-----VIIH 234
                                                                                                                                                                                                                                                                                      74 LYIVYEFLM-----SGWLSTYTWRCDPVDYSNSPEALRMVRVAWLFLF--SKFIELM 123
                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                  39 ADP--QYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILMNGALAAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 95274326; PubMed=7754713; Purnalle B., Coster F., Goffeau A.).

Purnalle B., Coster F., Goffeau A.).

The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for $24, a homologue to the aconitase gene AC01 and two homologues to chromosome III genes.";

Yeast 10:1235-1249(1994).

-!- FUNCTION: May be a membrane bound enzyme involved in the highly specific elongation of saturated 14-carbon fatty acids (14:0) to 16-carbon species (16:0).
                                                                                                               ENDOPLASMIC RETICULUM RETRIEVAL MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=96324909; PubMed=8702485;
Toke D.A., Martin C.E.;
"Isolation and characterization of a gene affecting fatty acid elongation in Saccharomyces cerevisiae.";
J. Biol. Chem. 271:18413-18422(1996).
                                            Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum.
TRANSMEM 23 43 POTENTIAL.
TRANSMEM 61 81 POTENTIAL.
                                                                                                                                                                      15.5%; Score 239; DB 1; Length 279; 28.7%; Pred. No. 7.5e-13; tive 47; Mismatches 97; Indels
                                                                                                                                                 B168EE4C7EAF92A6 CRC64;
                                                                                                                                 -> P (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-PEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation of fatty acids protein 1.
ELO1 OR YUL196C OR J0343.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                          POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                             235 LIWMYGTIFFMLFSNFWYHSY 255
Genew; HGNC:14418; ELOVL1.
InterPro; IPR002076; GNS1_SUR4.
PFfam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       LAFVIYVTFAILFIQFFVKAY
                                                                                                                                      68 68 5
279 AA; 32663 MW;
                                                                                                                                                                                  Local Similarity 28.7
nes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                         43
196
122
221
277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST
                                                                             TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                                                                        257
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
BLO1_YEAST
ID __BLO1_YEA
AC P39540;
                                                                                                                                                                                    Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 VYK--VKTEYKLPCQQ-----SVANLYLAFVIYVTFAILFIQFFVKAYIIKS-SKKSK 286
SUBCELLULAR LOCATION: Integral membrane protein (Potential). INDUCTION: Induced in wild type cells supplemented with 14:0 fatty acids and repressed when cells are supplied with 16- and 18-carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LYFILIKVIQKFMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 VGYTAVTWVPVTLNLAVHVLMYWYYPLSASGIRV--WWKAWVTRLQIVÖFMLDLIVVYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CYS---CNPTDVAAFWSFAFALSKIVELGDIMFIILRKRPLIFILHYYHHAAVLIYTVHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 AEHTAAGRFYILMMYYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ-MLAGVGITWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X77688; CAA54764.1; -.
EMBL; Z4541; CAA89491.1; -.
EMBL; Z4541; CAA89491.1; -.
BTR; S46638; S46638.
GermOnline; 141808; -.
SGD; S0003732; ELOI.
GO; GO:0019368; P:fatty acid elongase activity; IMP.
GO; GO:0019368; P:fatty acid elongation, unsaturated fatty acid; IMP.
INTERPO; IFROZO76; GNS1_SUR4.
PROSITE; PS01188; ELO; 1.
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P25358;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of fatty acids protein 2 (GNS1 protein) (v-SNARE bypass mutant gene 2 protein).
ELO2 OR FENI OR GNSI OR VEM2 OR YCR034W OR YCR521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyce cerevisiae (Baker, Byeast).

Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 14.3%; Score 220.5; DB 1; Length I Similarity 27.0%; Pred. No. 2.9e-11; 66; Conservative 48; Mismatches 111; Indels
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                                                                                                                                                                                                                                    SIMILARITY: Belongs to the ELO family.
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272
310 AA;
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                                                                                                                                                                                                                           MEDLINE=99054745; PubMed=9832547;
David D., Sundarababu S., Gerst J.E.;
Involvement of long chain fatty acid elongation in the trafficking of secretory vesicles in yeast.";
J. Cell Biol. 143:1167-1182(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diol. Chem. 272:17376-17384(1997).

-1- FUNCTION: Involved in synthesis of 1,3-beta-glucan. Could be a subunit of 1,3-beta-glucan synthesis. Could be also a component of the membrane bound fatty acid elongation systems that produce the 26-carbon very long chain fatty acids that are precursors for ceramide and sphingolipids. Appears to be involved in the elongation of fatty acids up to 24 carbons. Appears to have the highest affinity for substrates with chain length less than 22
                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=97362220; PubMed=9211877;
Oh C.-S., Toke D.A., Mandala S., Martin C.E.;
Oh C.S., Toke D.A., Mandala S., Martin G.E.;
"BLO2 and BLO3, homologues of the Saccharomyces cerevisiae ELO1 gene, function in fatty acid elongation and are required for sphingolipid
                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE-95286506; PubMed=7768822;
El-Sherbelini M., Clemas J.A.;
"Cloning and characterization of GNS1: a Saccharomyces cerevisiae gene involved in synthesis of 1.3-beta-glucan in vitro.";
J. Bacteriol. 177:3227-3234(1995).
                                                                                                                          MEDIINE=92133166; PubMed=1776366; Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P.; Wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P.; The complete sequence of a 7.5 Fb region of chromosome III from Saccharomyces cerevisiae that lies between CRY1 and MAT.";
      MEDINE=91181345; PubMed=1564349;
Thierry A., Fairhead C., Dujon B.;
"The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORFs, including a gene for a yeast ribokinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005783; C:endoplasmic reticulum; IDA.
GO; GO:0009922; F:fatty acid elongase activity; IMP.
GO; GO:0030497; P:fatty acid elongation; IMP.
GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
GO; GO:0030148; P:sphingolipid biosynthesis; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carbons.
SUBCELLUIAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the ELO family.
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Fatty acid biosynthesis; Transmembrane.
TRANSMEM 63 83 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56909; CAA40226.1; -.
EMBL; X59720; CAA42301.1; -.
EMBL; AF012655; AAB97766.1; -.
PIR; S12916; S12916.
GermOnline; 138940; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; S78624; AAB21260.1; -.
                                                                                   // (1990)
                                                                                                                                                                                  Weast 7:761-772(1991)
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                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                          78 YYVIİRGERFLISKSKPRKLNGLFQLHNLVLTSLSLTLLLLMVEQLVPIIVQHGLYPAIC 137
                                                                                                                                                                                                                                                                                                                                              122 YSCNPTDVAAFWSFAPALSKIVBLGDTWFIILRKRPLIFILHYYHH--AAVLIYTVHSGAE 179
                                                                                                                                                                                                                                                                                                                         180 HTAAGREYILMNYFAHSLMYTYYTVSAMGYRLPKGVSMTVTTVQTTQMLAGVG-ITWMVY 238
                                                                                                                                                                                                                                                                                      138 NIGAWTOPLVTLYYMNYIVKFIEFIDTFFLVLKHKKLTFLHTYHHGATALLCYTOLMGT- 196
                                                                                                                                                                                                                                                                                                                                                                                              239 KVKTEYKLP-----CQQSVANLYLAFVIYVTFALLFIQFFVKAYIIKSSKKSVK 289
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINEBALB/C; TISSUE-Liver;
MEDLINE=20253178; PubMed=10791983;
TVICH P., Westerberg R., Silve S., Asadi A., Jakobsson A., Cannon B.,
Loison G., Jacobsson A.;
FROIE Of a new mammalian gene family in the biosynthesis of very long chain fatty acids and sphingolipids.";
J. Cell Biol. 149:707-718(2000).
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                             14.
                                                                                                      Length 347;
                                                                                                      14.2%; Score 220; DB 1; Length 34 28.2%; Pred. No. 3.5e-11; ive 36; Mismatches 121; Indels
                                                                       24225E49A43A1003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELOZ MOUGE STANDARD; PRT; 292 AA.
Q9JIJ4; Q9DSZ;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of very long chain fatty acids protein 2.
ELOYL2 OR SSC2.
**Mus musculus (Mouse)
                 POTENTIAL. POTENTIAL.
                                                                         40002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2-292 FROM N.A.
                                                                                                                                              67; Conservative
 221
265
296
341
                 245
276
333
347 AA;
                                                                                                                           Similarity
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TRANSMEM
TRANSMEM
TRANSMEM
                                                         DOMAIN
SEQUENCE
                                                                                                            Query Match
Best Local
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ELO2 MOUSE
                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 YKTLCY---SCNPTDV---AAFWSFAFALSKIVELGDTMFIILRKR--PLIFLHYYHHAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNLOCONLDSAGEGDVRVAKVLWWYYP -- SKLVEFLDTIFFVLRKKTNOITFLHVYHHAS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V-----LIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPK-----WVSM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 MFNIWWCVLWWIPCGOSF-----FGPTLNSFIHILMYSYYGLSV----FPSMHKYLWWKK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 FVTTVQTTQMLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIFVTFAILFIQFFVKAY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 YLTQAQLVQFVLTITHT-LSAVVX-----PCGFPFGCLIFQSSYMMTLVILFLNFYIQTY 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELABEWNDLNTF--TIYGPNHTDMTTKYKYSYHFPGEQVADPQYWTILFQKYWYHSITIS 59
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                                                                                                                                                                                                                                                                                                                          .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reticulum (Potential):
TISSUE SPECIFICITY: Highly expressed in testis, lower level in liver. Weakly expressed in white adipose tissue, brain and kidney. SIMILARITY: Belongs to the ELO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF
FUNCTION: Could be implicated in tissue-specific synthesis of a long chain fatty acids and sphingolipids. May catalyze one or to of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl CoA
                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum TRANSMEM 30 50 POTENTIAL.
                                                                                                                                                                                                                                                                                             MGD; MGI:1858960; Elovi2.

GO; GO:0005792; C:microsome, IDA.

GO; GO:0016747; F:transferase activity, transferring groups of GO; GO:0000038; P:very.long-chain fatty acid metabolism; IDA.

InterPro; IPR002076; GNS1_SUR4.

PROSITE; PF01151; ELO; 1.

PROSITE; PF01151; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QİXAFDNEVNAFLDNMFGPRDSRVRGWFILDSYLP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E1959B8DFC43A7D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 219; DB 1;
Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL
                                                                                                                                                                                                                                                                    EMBL; AF170908; AAF72573,1; -. EMBL; AX014803; BAB29559.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 AA; 34207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIKSSKK---SKSVKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 RKKPVKKELQEKEVKN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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ID ELO2 HUMAN
AC Q9NXB9;
                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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TRANSMEM
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Best Local
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Ź 296

28-FEB-2003 (Rel. 41, Created)

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 LQCQDLTSAGEADIRVAKVLMWYYP.-SKSVEFLDTIFFVLRKKTSQITFLHVYHHASMF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LIYITVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPK-----WVSMTV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 ITVOTTOMLAGVGITWAVYKVKTEYKLPCQQSVANLYLAFVIYVTFALLFIQFFVKAXII 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 TQAQLVQPVLTITHT-MSAVVK-----PCGPPFGCLIPQSSYMLTLVILFLNFYVQTYRK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 TLCY---SCNPTDV---AAFWSFAFALSKIVELGDIMFIILRKR--PLIFLHYYHHAAV- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
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                                                                                                                                                                                                                                                                                                                            Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S., Submitted (FBB-2000) to the EmBL/GenBank/DDBJ databases.

-! PUNCTION: Could be implicated in tissue-specific synthesis of very long chain fatty acids and sphingolipids. May catalyze one or both of the reduction reaction in fatty acid elongation, i.e., conversion of beta-ketoacyl CoA to beta-hydroxyacyl CoA or reduction of trans-2-enoyl CoA to the saturated acyl COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LAEFWNDLNTF.-TIYGPNHTDMTTKYKYSYHFPGRQVADPQYWTILFQKYWYHSITISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TFFLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
ENDOPLASMIC RETICULUM RETRIEVAL MOTIF (POTENTIAL).
6FB735C4FBEC9FC1 CRC64;
                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derivative (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatty acid biosynthesis; Transmembrane; Endoplasmic reticulum. TRANSMEM 32 52 DOWENNINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 214; DB 1; Length 29 26.4%; Pred. No. 9.4e-11; ive 44; Mismatches 116; Indels
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation of very long chain fatty acids protein 2.
ELOVIZ OR SSC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reticulum (Potential).
-!- SIMILARITY: Belongs to the BLO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:14416; ELOVI.2.
InterPro; IPRO02076; GNS1_SUR4.
Pfam: PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 KSSKK-----SKSVKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK000341; BAA91096.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.4%;
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                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 AA;
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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260 KPMKKDMQEPPAGKEVKN 277

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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed=9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McKenney K., Adams M.D., Loftus B.,

Kirkness E.P., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Pujii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the UPF0182 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 102; DB 1; Length 880;
ilarity 19.3%; Pred. No. 0.58;
Conservative 47; Mismatches 83; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ransmembrane, Complete proteome.
41 POTENTIAL.
43 POTENTIAL.
124 POTENTIAL.
174 POTENTIAL.
217 POTENTIAL.
227 POTENTIAL.
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                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0182 protein AF1421.
                                                              880 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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HAMAP; MF 01600; -; 1.

Interpro; IPR005437; UPF0182.

Pfam; PF03699; UPF0182; 1.

Hypothetical protein; Transmembraransmam 19 41 P07

TRANSMEM 61 83 P07

TRANSMEM 103 125 P07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001005; AAB89825.1; -.
                                                              STANDARD;
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174
174
217
259
290
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268
280 AA;
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hes 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2234;
                                                          YE21 ARCFU
028851;
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SEQUENCE
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Matches
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47 LEGKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSID 106

107 PLR------SLYAEGFYKTLCYSCNPTDV------AAFWSFAFALSKIV 143

94

P, ઠે

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285
144 BLGDTWPIILRKRPLI------YHHAAVLI 171
                            212
                                                                                  248
                                                                                                                              154 -IGSLLAALLISLAIAAFAYMYAFRWVKSLEEFKEIFPGSGFWHFSALLPASFLLSAALI
                                                                               172 Y----TVHSGARH-TAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTT
                                                                                                             226 OMLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKS
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Search completed: June 16, 2004, 15:28:01 Job time : 18 secs

us-09-936-845a-15.rag

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein June 16, 2004, 15:21:03 , Search time 60 Seconds (without alignments) 1370.355 Million cell updates/sec Run on:

US-09-936-845A-15

1545 1 MELAEFWNDLMTFTIYGPNHPFVKAYIIKSSKKSKSVKNB 291 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1900s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

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	Description	Aab00198 Putative	Aab00199 Putative	Aab00205 Putative	Aae04173 Human gen	Abg92079 Human rec	O Human	Abb78813 Human NOV	Human	Abp56418 Human elo	Abb82960 Human LCE		Aay79263 Putative		Abb60310 Drosophil		Aae04172 Human gen	Aay79260 Putative	Aab48959 Mouse fat	Abp56420 Human elo	Aay79249 Human put	_	Aay79264 Putative	App56419 Human elo	Abb82959 Human LCE	Abb78814 GNS1/SUR4
SUMMAKIRS	. di	AAB00198	AAB00199	AAB00205	AAE04173	ABG92079	AAE24550	ABB78813	ABB78812	ABP56418	ABB82960	ABB82966	AAY79263	AAU87829	ABB60310	AAE37330	AAE04172	AAY79260	AAB48959	ABP56420	AAY79249	AAB00209	AAY79264	ABP56419	ABB82959	ABB78814
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56	27	28	53	30	31	32	33	34	35	36	37	38	di M	40	41	42	43	44	45

ALIGNMENTS

Blongase; polyunsaturated fatty acid; PUFA; dietary supplement; pharmaceutical; foodstuff; food; di-homo-gamma-linoleic acid; arachidonic acid; eicosapentanoic acid; docosatrienoic acid; docosatetraenoic acid; docosatetraenoic acid; Putative polyunsaturate fatty acid elongase (PUFA). AAB00198 standard; protein; 291 AA (first entry) 08-FBB-2001 AAB00198; RESULT 1 AAB00198

Caenorhabditis elegans. WO200055330-A1

21-SEP-2000.

20-MAR-2000; 2000WO-GB001035.

18-MAR-1999; 99GB-0006307. 18-FBB-2000; 2000GB-00003869.

(UYBR-) UNIV BRISTOL.

Napier JA;

WPI; 2000-647074/62.

Novel isolated polypeptide comprising functional long chain polynnsaturated fatty acid (PUPA) elongase of Caenorhabditis elegans used to produce PUPA for foodstuff, dietary supplement or pharmaceutical composition.

Disclosure; Page 25; 42pp; English.

New elongase polypeptides which are functional long chain polyunsaturated fatty acid (PUFA) elongase polypeptides are described. The elongase catalyses an elongase reaction to produce PUFA (24 carbon fatty acid with at least 4 double bonds) such as di-homo-gamma-linoleic acid (20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), elocaspentanoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid (22:3Delta3,16,19), docosaterraenoic acid (22:3Delta3,16,19) or docosateraenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid (22:5Delta7,10,13,16,19) or docosahexaenoic acid (22:6Delta4,7,10,13,16,19). PUFA produced is useful in foodstuffs,

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compositions which can then
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                                                                                                                                                                                                                                                                                                                                                                                                      Elongase; polyunsaturated fatty acid; PUFA; dietary supplement; pharmaceutical; foodstuff; food; di-homo-agamma-linoleic acid; arachidonic acid; elcosapentamoric acid; docosatrienoic acid; docosatertaenoic acid; docosatertaenoic acid; docosatertaenoic acid;
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                                                 100.0%; Score 1545; DB 3;
100.0%; Pred. No. 2.7e-161;
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 supplements and in pharmaceutical elavate PUFA levels of an animal o
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                                                                     Matches 291; Conservative
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(20:3Delta8,11,14), arachidonic acid (20:4Delta5,8,11,14), eicosapentanoic acid (20:5Delta5,8,11,14,17), docosatrienoic acid (22:3Delta3,16,19), docosatetraenoic acid (22:4Delta7,10,13,16,19) or docosabentaenoic acid (22:5Delta4,7,10,13,16,19) or docosabexaenoic acid (22:5Delta4,7,10,13,16,19). PUFA produced is useful in foodstuffs, dietary supplements and in pharmaceutical compositions which can then lused to elavate PUFA levels of an animal or plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 TLQLAQMVMGVIIGVTVYRIKSSGEY---CQQTWDNLGLCFGVYPTYPLLFANFPYHAVV
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                                                                                                                                                                                                                                  36.5%; Score 564; DB 3;
42.0%; Pred. No. 4.4e-53;
iive 45; Mismatches 86
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                                                                                                                    Novel isolated polypeptide comprising functional long chain polyunsaturated fatty acid (PUFA) elongase of Caenorhabditis elegans used to produce PUFA for foodstuff, dietary supplement or pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 SITISVLYFILIKVIQKFWENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 GFYKTLCYSCNPTDVAAFWSFAFALSKIVELGDTWFIILRKRPLIFLHYYHHAAVLIYTV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                            35.4%; Score 547; DB 3; Length 269; 42.4%; Pred. No. 1.7e-51; tive 39; Mismatches 88; Indels 4
                                                                                                                                                                                                 Disclosure, Page 27, 42pp, English,
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18-FEB-2000; 2000GB-00003869.
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Les 123; Conservative
                              (UYBR-) UNIV BRISTOL
                                                                                         WPI; 2000-647074/62.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 269 AA;
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                                                                                                                                                                     composition.
                                                             Napier JA;
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AMONGHOWANDOMATOR represent CDNAs corresponding to 24 human secreted protein genes, and AAE04100-AAE004170 represent the proteins they encode. AAE041101-AAE004100-AAE004170 represent the protein states. The secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted profetines can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include caveloping products for the diagnosis or treatment of proliferative disorders, theorems, foetal and developmental abnormalities. Caveloping products for the firmulation, allerative disorders, diseases of the immune system, AIDS, autoimmune constitute disorders, diseases of the immune system, AIDS, autoimmune disorders, diseases (e.g., rheumatoid arthritis), inflammation, allerative committee disorders, schizophrenia, asthma, skin disorders. (e.g., Alzheimer's disease, Parkinson's disease), committee disorders, achizophrenia, skin disorders. (e.g., argiophrenia, asthma, skin disorders.) argiophrenia, asthma, skin disorders. (e.g., argiophrenia, achma, skin disorders.) argiophrenia, achma, skin disorders, cordivoracular disorders, proteins can also be used to aid wound healing and epithelial cell corteins can also be used to aid wound healing and epithelial cell or proteins can also be used to aid wound healing and epithelial cell or a protein of the invention can be used as a food additive or argines, and continue of primary tissues, correctine of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in disagnostic immunoassay or enzyme linked immunosorbent assay (Elizabent sequence represents a human secreted protein fragment represents a human secreted protein fragment effections.
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                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 24 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                              Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes mellitus and multiple sclerosis.
                                                                                                                                                                                                                              Komatsoulis GA, Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 7; 532pp; English.
12-NOV-1999; 99US-0164825P.
03-AUG-2000; 2000US-0222904P.
                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                     WPI; 2001-374441/39.
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Human, receptor and membrane-associated protein; REMAP; atherosclerosis; cardiovascular disorder; hypertension; congestive heart failure; oedema; aneurysm; angina pectoris; ischaemic heart disease; lung disease; nausea; rheumatic heart disease; nancea; archeumatic heart disease; chronic obstructive pulmonary disease; astema; emphysema; bronchitis; gastrointestinal disorder; peptic ulcer; asthma; crohn's disease; lipid metabolism disorder; Fabry's disease; dementia; pancreatitis; diabetes mellitus; hyperlipidaemia; autoimmune disorder; inflammatory disorder; neurological disorder; Creutzfeldt-Jakob disease; cell proliferative disorder; protein replacement therapy; adenocardinoma; developmental disorder; metabolic disorder; Alzheimer's disease; stroke; Parkinson's disease; multiple sclerosis; Cushing's syndrome; anxiety; schizophrenia; Addison's disease; endocrine disorder; gene therapy; gout; amnesia; cancer; leukaemia; lymphoma; myeloma; sarcoma.
MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYI---IKSSK 283
                                   New human receptor and membrane-associated proteins and polynucleotides, useful for diagnosing, treating or preventing cardiovascular disorders (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Azimzai Y, Yue H, Ding L, Nguyen DB, Gandhi AR, Burford N; Thangavelu K, Elliott VS, Ramkumar J, Yao MG, Lal PG, Tang TY; Swarnakar A, Warren BA, Walia NK, Policky UL, Ku Y, Honchell CD; Au-Young J, Baughn MR, Duggan BK, Lu DAM, Gietzen KJ, Hillmann JL; Raumann BE, Lu Y, Sapperetein SK, Tran UK, Richardson TW; Emerling BM, Hafalia AJA, Burrill JD, Marcus GA, Zingler KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human receptors and membrane associated protein REMAP-22.
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                                                                                                                                                                                                                                                                                                                                                                                                                   ABG92079 standard; protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2001; 2001US-0269580P. 09-APR-2001; 2001US-0282679P.
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14-JAN-2002; 2002US-0348687P.
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N-PSDB; ABS67800.
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                                                                                                                                                       284 KSK 286
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Kable AE,
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                                                                                                                                                                                                                                                                                                                                                                               ABG92079
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The present invention relates to a new receptor and membrane-associated protein (REMAP). The polypeptide, polynucleotide and agonist are useful for treating a condition associated with decreased expression of functional REMAP. The antagonist is useful for treating a disease associated with overexpression of functional REMAP. The anti-REMAP

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the expression of REMAP. These polypeptides, polymucleotides, agonists and antagonists are particularly useful for diagnosing, treating or preventing cardiovascular (e.g. atherosclerosis, pypertension, aneuryems, preventing cardiovascular (e.g. atherosclerosis, pypertension, aneuryems, congestive heart failure, angina pectoris, or ischaemic or rheumatic congestive heart failure, angina pectoris, or ischaemic or rheumatic congestive branchitis) gastrointestinal (e.g. nausea, peptic ulder or crohn's disease, lipid metabolism (e.g. Rabry's disease, diabetes conflicts or hyperlipidaemia, autoimmune/inflammatory (e.g. anaemia, cathma, gout, pancreatitis or Crohn's disease, nauchogical (e.g. antenia) stroke, Alzheimer's disease, creutzfeldt-Jakob disease, caming stroke, Alzheimer's disease, anxiety, schizophrenia or multiple sclerosis, parkinson's disease, anxiety, schizophrenia or cubling's syndrome), endocrine or cell proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, myeloma or sarcoma). The present amino acid sequence represents a human REMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 MFVGAIVSILTYIMRQDQ--GCHTTMEHLFWSFILYMTYFILFAHFFCQTYIRFKVKAKT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; elongase; therapy; enzyme; polyunsaturated fatty acid; sinusitis; purp, disorder; cardiovascular disorder; articular cartilage degradation; peripheral vascular disease; atheroseleroseis, coronary artery disease; inflammatory disorder; panoreatitis; asthma; gastrointestinal disorder; osteoarthritis; rheumatoid arthritis; congenital liver disease; cancer; acne; sigoren's syndrome; body weight disorder; creebrovascular disease; acute respiratory distress syndrome; hypercholesterolaemia; alcoholism; postviral fatigue; psychiatric disorder; pre-menetrual syndrome; eczema; Altaeimer's syndrome; hyperriglyceridaemia; cyetic fibrosis; anorexia; autoimmune disorder; obesity; cachexia; viral disease; endometriosis; dyslipidaemia; atopic disorder; diabetes; ELG6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 GTVLITGGLKQTVCFINFIDNSTVKFWSWVFLLSKVIBLGDTAFILLKKRPLIFIHWYHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%; Score 492; DB 5; Length 270; 39.9%; Pred. No. 2e-45; ive 53; Mismatches 87; Indels
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Best Local Similarity 39.97
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 270 AA;
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The invention relates to movel elongase polypeptides, genes and their control regions. Sequences of the invention are used in the diagnosis and treatment of polympaturated fatty acid (PPIPA) disorders such as cardiovascular disorders (e.g. sinusitis, pancreatitis, asthma, osteoarthrisis, rheumatorid arthritis, acne), Sjogren's syndrome, body of posturiral fatigue, gastrointestinal disorders, eczema, psychiatric disorders, cancer, congenital liver disease, alcoholism, Alzheimer's syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome, syndrome, cystic fibrosis, endometriosis, pre-menstrual syndrome, hypercholesterolaemia, hypertrialyceridaemia, dyslipidaemia, peripheral vascular disease, cerebrovascular disease, autoimmune disorders, acute respiratory distress syndrome, atopic disorders, articular cartilage degradation, diabetes and diabetic complication. The present sequence is human elongase (ELG6) protein
                                                                                                                                                                                                                                             Novel elongase polypeptide, genes and their control regions useful in determining compositions for treating polyunsaturated fatty acid disorder e.g. cardiovascular, inflammation, gastrointestinal disorders and cancer.
                                                                                                                       De Antueno RJ, Jenkins DK;
                                                                                                                     Haardt M, De Antuel
ton A, Goldberg YP;
                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 160-161; 173pp; English.
                                                                                                                                              Ponton A,
29-NOV-2001, 2001WO-CA001705
                                     29-NOV-2000; 2000US-0253728P
                                                                               (XENO-) XENON GENETICS INC
                                                                                                                          Knickle LC,
                                                                                                                                         Allen SJ,
                                                                                                                                                                                   WPI; 2002-547693/58.
                                                                                                                                                                                                          N-PSDB; AAD42270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 270 AA;
                                                                                                                          Winther MD,
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POKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107 108 IRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTWFIILRKRPLIFLHYYHH 166 167 AAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226 MLAGUGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTPAILFIQ?FVKAYI---IKSSK 283 STYLVYTSFGYKNKVPAGGWFVTMNFGVHAIMYTYYTLKAANVKPPRMLPMLITSLQILQ 9 DB 5; Length 270; 87; Indels 31.8%; Score 492; DB 5; 39.9%; Pred. No. 2e-45; tive 53; Mismatches E Conservative Local Similarity KSK 286 . 16 210 48 39 90 150 227 284 Query Match Matches 셤 셤 쉱 ò g ò ठे ò දි

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Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer;
                                                                                           Human NOV6b protein sequence SEQ ID NO:20.
              Ą
              ABB78813 standard; protein; 270
                                                                  (first entry)
                                                                  29-JUL-2002
                                         ABB78813;
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KSQ 270

cardiomyopathy, atherosclerosis, cell signal processing, diabetes; AIDS; metabolic pathway modulation, neoplastic, neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn's disease; multiple sclerosis; Graft versus host disease; 2000US-0240625P. 2000US-0240637P. 2000US-0240648P. 2000US-0240669P. 12-OCT-2001; 2001WO-US031922 2000US-0240113P 2000US-0240732P 2000US-0241190P WO200230974-A2 16-OCT-2000; 16-OCT-2000; 16-OCT-2000; 16-OCT-2000; chromosome 10. Homo sapiens. .6-OCT-2000; 12-OCT-2000; 16-OCT-2000; 18-APR-2002

Alsobrook JP, Lepley DM, Burgess CE, Mishra V; Ji L, Padigaru M, Shimkets RA, Zerhusen BD, Spytek KA; Gerlach V, Macdougall J, Stone D, Gunther E, Bllerman K; Ξ Grosse WM, Kekuda R, Edinger S,

2001US-0262455P

18-JAN-2001;

CURAGEN CORP. MILLET I.

(MILL/) CURA-)

WPI; 2002-444172/47. N-PSDB; ABNB6919.

New NOVX polypeptides and polymucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes.

Claim 1; Page 53; 227pp; English.

The present invention describes novel human proteins designated NOVX (Where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrotein xinase e-like protein; NOV2-d are Keratin 4-like protein; NOV2-d are Keratin B-like protein; NOV3 is a collagan-like protein; NOV4 is a matrilin-like protein; NOV9 is a matrilin-like protein; NOV9 is a matrilin-like protein; NOV9 is a tyrosprotein 30-like protein; NOV7 is a matrilin-like protein; NOV9 is a tyrosprotein 30-like protein; NOV9 is a tyrosprotein 30-like protein; NOV9 is a tyrosprotein; and is a tyrosprotein 30-like protein; NOV9 is a tyrosprotein; and coll in the protein and to the protein; NOV9 is a tyrosprotein and like protein. NOV9 sequences have cytostatic, anticipating and electric and is an end of sorder or a pathological concenting or alleviating and NOV4-associated disorder or apathological concessing and metabolic pathway modulation or diabetes. The NOV7 sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOV7 sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOV7 sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOV7 concessing and metabolic pathway modularly accer. The NOV7 sequences are also useful for determining the treatment of especially useful in therapeutic or prophylactic applications for response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft response, AIDS, asthma, NoV6b is located to chromosome 10 concentration from the present invention. NOV6b is located to chromosome 10 concentration from the present invention.

Gape 9 31.8%; Score 492; DB 5; Length 270; 39.9%; Pred. No. 2e-45; ive 53; Mismatches 87; Indels Local Similarity 39.9 es 97; Conservative Query Match Best Loca Matches

Seguence 270 AA;

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227pp; English.

52;

Claim 1; Page

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GTVLITGGLKQTVCFINFIDNSTVKFWSWVFLLSKVIBLGDTAFILLRKRPLIFHWYHH 149
                                                                                                      226
                                                                                                                      STVLVYTSFGYKKKVPAGGWFVTWNPGVHAIMYTYYTLKAANVXPPKMLPMLITSLQILQ 209
                                                                                                                                                                         FOKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                         MEAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFAILFIQPFVKAYI---IKSSK 283
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, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic, immunosuppressive; neuroprotective; gene therapy; cancer; cardicomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn's disease; multiple sclerosis; Graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                              NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma;
                AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ
                                                    LRSLYAEGEYKTLCY-SCNPTDVAAFWSFARALSKIVELGDTMFIILRKRPLIFLHYYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burgess CE, Mishra V
s RA, Zerhusen BD, S
Stone D, Gunther E,
                                                                                                                                                                                                                                                                                                                                                                                     Human NOV6a protein sequence SEQ ID NO:18.
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Li L, Padigaru M, Shimkets
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h V, Macdougall J,
                                                                                                                                                                                                                                                                                                          ABB78812 standard, protein; 270 AA.
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16-OCT-2000, 2005US-02406379.
16-OCT-2000, 2005US-02406489.
16-OCT-2000, 2005US-02406629.
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16-0CT-2000; 2000US-0240703P
16-0CT-2000; 2000US-0240732P
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(MILL/) MILLET I.
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Kekuda R, I
Edinger S,
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The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like protein; NOV3 is a collagen-like protein; NOV4 is a cystatin B-like coprotein; NOV5 is a serotonin receptor-like protein; NOV6 is a matrilin-2-like protein; NOV9 is a matrilin-2-like cold inducible glycoprotein 30-like protein; NOV9 is a matrilin-2-like protein; NOV9 is a tyrosine kinase-like protein; NOV9 is a protein; NOV9 is a tyrosine kinase-like protein; NOV9 is a protein; NOV9 is a cardiovagenty, a dicardiovascular, antidiabetic, immunosuppressive and cardiomyopathy, atherosclerosis, a disorder related to cell signal cardiomyopathy, atherosclerosis, a disorder related to cell signal proteins are also useful for determining the presence of or proteins protein mucleic acid, particularly cancer. The NOVX sequences are collapsed in therapeutic or prophylactic applications for morphasic or neurological disorders, and in the treatment of emembers immine interner and interner and interner and interner immine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 LRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQFTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, AIDS, atthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence represents the human NOV6a protein from the present invention. NOV6a is located to chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.8%; Score 492; DB 5; Length 270; 39.9%; Pred. No. 2e-45; ive 53; Mismatches 87; Indels
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Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 270 AA;
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New isolated human elongase HSELO1-like polynucleotide and encoded peptide, useful for treating, preventing and ameliorating diseases such as COPD, cancer, metabolic disease, diabetes, CNS disorders, or asthma.
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39.9%; Pred. No. 2e-45;
iive 53; Mismatches |
                                                                                                          WPI; 2002-636596/68.
N-PSDB; ABZ22162, ABZ22164, ABZ22165.
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                                                                                                                                                                 Claim 25; Fig 2; 128pp; English.
                                             07-FEB-2002; 2002WO-EP001262
                                                           08-FEB-2001; 2001US-0267135P
                                                                                                                                                                                                                                                                                                                                              97; Conservative
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Best Local Similarity
Matches 97; Conserv
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                                                                           (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                               Sequence 270 AA;
              WO200262974-A2.
Homo sapiens.
                            15-AUG-2002
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The invention relates to identifying a candidate p53 pathway modulating agent that involves assaying a purified LCE (long chain fatty acylelogaes) polypeptide or nucleic acid or its functionally active fragment or derivative, with a test agent. The methods are useful for identifying a candidate p53 pathway modulating agent, modulating a p53 pathway of a candidate p53 pathway modulating agent, modulating a p53 pathway of a candidate branching morphogenesis modulating agent, and modulating branching morphogenesis in adminish cell. The diseases that can be diagnosed are breast, colon, lung or ovary cancer having greater than 25% expression level. The method is useful for manufacturing a medicament for diagnosing or treating breast, colon, lung or ovary cancer. Sequences ABB82959-966 represent human LCE related polypeptide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a candidate p53 pathway modulating agent for diagnosing/treating cancer comprises detecting a test agent-biased activity of an assay system comprising a purified long chain fatty acylelongase (LCE) polypeptide or nucleic acid.
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                                                              LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Francis-Lang H,
                   Human LCE related protein (sequence ID No. 10)
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Koblizek TI;
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10-OCT-2001, 2001US-0328605P.
15-FEB-2002, 2002US-0357253P.
01-MAR-2002, 2002US-0361196P.
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Best Local Similarity 39.95
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman GD,
                                                                                           cancer; human; enzyme
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                                                                                                                                                                                  WO200299068-A2
                                                                                                                                        Homo sapiens.
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(I) has cytostatic, antidiabetic, antiasthmatic, anti-HIV, nootropic, antiparkinsonian, neuroprotective, tranquilliser, antimigraine, and present an algebra sequence of the sequence of a disease, and can be used in gene therapy. (I) can be used in the treatment of a disease, such as cancral nervous system (CRS) disorder, satchma, metabolic disease or COPD. The human elongase HSELO1-like protein is useful in preventing, treating or ameliorating the diseases cited above, including Parkinson's disease, dementia, multiple solerosis, stroke, HIV, alzeeiner's disease, Huntington's disease, Creutzfeldt-Jakob disease, schizophnenia, psychosis, attention deficit disorders, pain associated with CNS disorders, with cancer, or headache pain, e.g. migraine. It can also be useful in identifying test compounds that may act as activators or inhibitors at the enzyme's active site, or in raising specific antibodies that can block and effectively reduce its activity
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Funke

Li D,

166

KSQ 270

268

(first entry)

14-APR-2003

g 8

Gaps

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This sequence is that of a putative Drosophila melanogaster homologue, termed DMI, of Mortierella alpina polyunsaturated fatty acid (BUFA) telongase GELELO (See ANY9243). It is the translation of a DNA fragment identified in a database search using GLELO as query. The 2 sequences show 27.2% identity in a 206 amino acid overlap. The invention provides PUPA elongase mulloleoide sequences and polypeptides that are involved in the elongation of PUFAs, such as gamma-linolenic acid. The invention also provides host cells, transgenic plants and transgenic animals expressing an elongase, and methods for production of PUFAs, such as dihomo-gamma-linolenic acid and elocacatetraemoic acid, for use in nutritional, pharmaccutical, cosmetic and animal feed compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 KPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCYS--CNPTDVAAFWS 134
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210 MFVGAIVSILTYIWRQDQ--GCHTTWEHLFWSFILYMTYFILFAHFFCQFYIRPKVKAKT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blongase; GLELO; polyunsaturated fatty acid; eicosatetraenoic acid; dihomo-gamma-linolenic acid; transgenic plant; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids encoding elongase enzymes for producing polyunsaturated fatty acids that can be used to form nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative Drosophila melanogaster homologue of elongase GLBLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thurmond J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "unidentified residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key Location/Qualifiers Misc-difference 235
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                                                                                                                                                                                                                                                                                     AAY79263 standard; protein; 278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US019715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 278 AA;
                                                               KSK 286
                                                                                                                        268 KSQ 270
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                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a candidate p53 pathway modulating agent for diagnosing/treating cancer comprises detecting a test agent-biased activity of an assay system comprising a purified long chain fatty acylelongase (LCB) polypeptide or nucleic acid.
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                                                                                                                                                                                                                                                                                                                          LCE; long chain fatty acyl elongase; p53; cytostatic; gene therapy;
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                                                                                                                                                                                                                                                          Human LCE related protein (GenBanK Identifier No. GI#17454617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman GD, Belvin M, syes LN, Koblizek TI;
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                                                                         ABB82966 standard; protein; 270 AA.
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10-0CT-2001; 2001US-032860SP.
15-PEB-2002; 2002US-0357253P.
01-MAR-2002; 2002US-0361196P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2002; 2002WO-US017739
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                                                                                                                                                                                                                                                                                                                                                              cancer; human; enzyme
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                                                                                                                                         ABB82966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elongase; polyunsaturated fatty acid; pufa; transgenic plant; transgenic plant; transgenic non-human animal; plant oil; arachidonic acid; nutritional; pharmaceutical; cosmetic; and faced; restenceis; angioplasty; AIDS; acquired immunodeficiency syndrome; multiple sclerosis; cachexia; asthma; fill lammacrory skin disease; osteoporosis; kidney stone; canner; eczema; inflammation; rheumatoid arthritis; psoriasis; platelet aggregation; vasodilation; cholesterol reduction; gastrointestinal bleeding.
   FAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                   HSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI-TWMVYKVKTEYKLPCQQSVA 253
                                                                                                                                                       Isolated nucleic acid sequences encoding elongase proteins, useful in the production of polyunsaturated fatty acids, e.g. arachidonic acid, which can then be used nutritional compositions and pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated nucleic acid sequences encoding
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                                                                                                                                                                                                                                                                                  NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Fig 41; 271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU87829 standard; protein; 278 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fruitfly GLELO homologue DM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-2001; 2001WO-US023259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-2000; 2000US-00624670.
11-JUL-2001; 2001US-00903456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-172011/22.
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Thurmond J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       62
useful for inhibiting platelet aggregation, inducing vasodilation, reducing cholesterol, reducing or preventing gastrointestinal bleeding and side effects of non-steroidal anti-inflammatory drugs. The present sequence represents an elongase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : | | : | | : | | : | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 WLFVLSKLPELGDFIFIVLRKQPLIFLHWYHHITVLIYSWFSYTEYTSSARWFIVMNYCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 KPFTLKYPLILWNGALAAFSIIATLRPSIDPLRSLYAEGFYKTLCYS--CNPTDVAAFWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI - TWMVYKVKTEYKLPCQQSVA
                                                                                                                                                                                                                                                                                                                                                                          23 MITKYKYSYHFPGEQVADP----QYWTILFQKYWYHSITISVLYFILIKVIQKFMENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                         Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, SEQ ID NO 7722; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                              31.4%; Score 485.5; DB 5
37.7%; Pred. No. 1.1e-44;
ive 54; Mismatches 99
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                     Seguence 278 AA;
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                                                                                                                                                                                                                                                                                                      103;
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                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                             PAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                             9,
                                                                                                                                                                                                                        26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to very long chain fatty acid (VLFA) biosynthesis
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL36175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                PRFQLRGPLIIWNTLLAMPSIMGAARTAPELIHVLRHYGLFHSVCVPSYIBQDRVCGFWT
                                                                                                                                                                                             MITKYKYSYHFPGEQVADP-----QYWIILFQKYWYHSITISVLYFILIKVIQKFMENR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; very long chain fatty acid biosynthesis enzyme; VLPA; VLCPABB; non-insulin dependent diabetes mellitus; NIDDW; adresnleukodystrophy; ALD; autosomal dominant macular dystrophy; addm; Alzheimer's disease; coronary heart disease; stroke; myocardial infarction; gene therapy.
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid molecule comprising a very long chain fatt; acid biosynthesis enzyme nucleic acid, useful for treating a disease associated with the biosynthesis enzyme nucleic acid.
                                                                                                                                                               17;
                                                                                                                                   Length 313;
                                                                                                                                                               Indels
                                                                                                                                   Query Match 31.4%; Score 484.5; DB 4;
Best Local Similarity 37.7%; Pred. No. 1.6e-44;
Matches 103; Conservative 54; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human VLCFABE MOOSE00004 protein from ctg13284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE37330 standard; protein; 263 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-2002; 2002WO-IB004610
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                                                                                                      Sequence 313 AA;
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                              (ALD)
    Sequences
enzymes (VLCFABE) and polynucleotides encoding such proteins. Sequences of the invention are useful for treating VLCFABE diseases such as non-insulin dependent diabetes mellitus (NIDDM), adrenoleukodystrophy (ALD) autosomal dominant macular dystrophy (admb), Adrheimer's disease and coronary heart diseases such as stroke and myocardial infarction. They are also used in gene therapy. The present sequence is human VLCFABE
                                                                                                                                                                                                                                                                                              TMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAM
                                                                                                                                                                                                                                                                                                                                                    29 YSYHPPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILW
                                                                                                                                                                                                                                                                         89 NGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCY-SCNPTDVAAFWSFAFALSKIVELGD
                                                                                                                                                                                                                                                                                                                                                                                              208 GYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFAI
                                                                                                                                                                                  Gaps
                                                                                                                                                                                  13;
                                                                                                                                                   Length 263;
                                                                                                                                                                                  Indels
                                                                                                                                                       DB 6;
                                                                                                                                                     31.3%; Score 483.5; DB 6; 37.5%; Pred. No. 1.6e-44; iive 55; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 LFIQPFVKAYI---IKSSKKSKSVKNE 291
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1 MELAEFWNDLNTFTIYGPNH.....PFVKAYIIKGSKKSKSVKNB 291
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1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*
3: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 5831, Ap Sequence 18, Appl Sequence 20, Appl Sequence 58, Appl Sequence 58, Appl Sequence 53, Appl Sequence 107, App Sequence 107, Appl Sequence 53, Appl Sequence 24, Appl Sequence 27, Appl Sequence 21, Appl Description 0 US-09-976-782-18 0 US-09-976-782-18 0 US-09-976-782-20 0 US-09-903-456-58 4 US-10-156-911-58 4 US-10-156-911-58 4 US-09-903-456-54 0 US-09-976-782-107 1 US-09-903-456-54 1 US-10-156-911-53 4 US-10-156-911-54 4 US-10-156-911-24 8 Query Match Length 744 864 8686 46 Score Result No.

120

61 LYPILIKVIQKFMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL

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Sequence 9, Application US/10433238
Publication No. US20040086899A1
GENERAL INFORMATION:
APPLICANT: Winther, Michael D
APPLICANT: Wintcher, Leah C
APPLICANT: Haardt, Martin
APPLICANT: Haardt, Martin
APPLICANT: Alan, Stephen J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-976-782-20
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CURRENT PILLING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR APPLICATION NUMBER: 60/240,662
PRIOR PAPLICATION NUMBER: 60/240,665
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,703
PRIOR APPLICATION NUMBER: 60/240,669
PRIOR PLING DATE: 2000-10-16
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                                              TAAGREYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKV 240
                                                                          30 FEEYWATSFPIALIYIVULAAVQQNYMKERKGFNLQGPLILMSFCLAIFSILGAVRAMGIM 89
                                                                                                                                    KTEYKLPCQQSVANLYIAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVKNE 291
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                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09976782
Publication No. US20030190715A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 20, Application US/09976782
Publication No. US20030190715A1
GRNEAL INFORMATION:
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GRNEAL TITLE OF INVENTION:
OUTREAT PELLICATION NUMBER:
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Best Local Similarity 39.9%; Pred. No. 8.6e-43;
Matches 97; Conservative 53; Mismatches 87;
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i LOCATION: {235}...(235)
i OTHER INFORMATION: Xaa = Unknown or Other at position 235
US-09-903-456-58
                                                                                  Query Match
Best Local Similarity 37.7%
Matches 103; Conservative
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US-10-156-911-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 MFVGAIVSILTYIWRQDQ--GCHTTWEHLFWSPILYMTYFILFAHFFCQTYIRFKVXAKT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 FOXYWYHSITISVLYPILIKVIOKFWENRKPPTLKYPLILWNGALAAFSIIATLRFSIDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 FEEYWAISPPIALIYLVLIAVGQNYMKERKGFNLQGPLILMSFCLAIFSILGAVRMWGIM 89
APPLICANT: Ponton, Andre
APPLICANT: De Antueno, Roberto J
APPLICANT: De Antueno, Roberto J
APPLICANT: Jenka, S.olomon O
APPLICANT: Waska, S.olomon O
APPLICANT: Goldberg, Y Paul
TITLE OF INVENTION: Human Elongase Genes, Uses Thereof, and Compounds for
TITLE OF INVENTION: Wodulating Same
FILE REPERRACE: 330339-00004
CURRENT PAPLICATION NUMBER: US/10/433,238
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: US 60/253,728
PRIOR FILING DATE: 2000-011-29
NUMBER: OF SEQ ID NOS: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 GTVLIGGLKQTVCFINFIDNSTVKFWSWVFLLSKVIELGDTAFILLRKRPLIFIHWYHH
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Patent No. US2002013834A1

GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Headray Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 640.708.P3

CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
FRIOR FILING DATE: 2001-07-11
FRIOR PLING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 1999-09-23
FRIOR FILING DATE: 1999-09-23
FRIOR FILING DATE: 1999-09-23
FRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
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ORGANISM: Drosophila melanogaster
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Best Local Similarity 39.9%
Matches 97; Conservative
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CRGANISM: human
US-10-433-238-9
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LENGTH: 278
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                                                                                                                                                                                                                                     63 PRPQLRGPLIIMNTLLAMFSIMGAARTAPELIHVLRHYGEFHSVCVPSYIEQDRVCGFWT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                          135 FAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                                                                                                                                                                HSLMYTYYTVSAMGYRLPKAVSMTVTTVQTTQMLAGVGI-TWMVYKVKTBYKLPÇQQSVA 253
                                                                                                                                                                                                  77 KPFTLKYPLILWNGALAAFSILATLRFSIDPLRSLYAEGFYKTLCYS--CNPTDVAAFWS 134
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                                                                                                                                  11 VTPNYSYIFDFENDFIHQRTRKWMLENWTWVF---YYCGI-----YKLVIFGGQHFMQNR 62
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                                                                                                     23 MITKYKYSYHFPGEQVADP-----QYWIILFQKYWYHSITISVLYFILIKVIQKFMENR
                                                     Gaps
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Length 278;
  31.4%; Score 485.5; DB 9; Length 2 37.7%; Pred. No. 4.3e-42; tive 54; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch al Similarity 37.7%; Pred. No. 4.3e-42; 103; Conservative 54; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: (235)...(235) CTHER INFORMATION: Xaa = Unknown or Other at position 235 US-10-156-911-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 6407.US.P4
CURRENT APPLICATION NUMBER: US 09/903.456
FRICH APPLICATION NUMBER: US 09/903.456
FRICH RILING DATE: 2001-07-11
FRICH APPLICATION NUMBER: US 09/379,095
FRICH RILING DATE: 2000-07-24
FRICH RILING DATE: 12000-07-24
FRICH APPLICATION NUMBER: US 09/145,828
FRICH RILING DATE: 1998-09-02
NUMBER: OF SEQ ID NOS: 122
SOFTWARE: FESTERE OF CIT WINDOWS VETSION 4.0
SEQ ID NO 58
LENGTH: 278
LENGTH: 278
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ORGANISM: Drosophila melanogaster
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US-09-976-782-107
 US-09-903-456-53
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63 PRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVGGFWT 122
                                                      HSIAMYTYYTVSAMGYRLPKWVSMTVŢTVQTTQMLAGVGI-TWMVYKVKTBYKLPCQQSVA 253
                                                                                                                         135 PAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (235)...(235)
CTHER INFORMATION: Xaa = Unknown or Other at position 235
US-10-408-736-56
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                                                                                                                                                                         NEYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                               243 NINLSIAMYSSYPVLFARFFYKAYLAPGGHKSR 275
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Table, Taples APPLICANT: Table APPLICANT: Parker-Barnes, Jennifer M. APPLICANT: Parker-Barnes, Jennifer M. APPLICANT: Parker-Barnes, Jennifer M. APPLICANT: Leonard, Jennifer M. TITLE OF INVENTION: ELOCASE GENES AND USES THE TITLE REFERENCE: 6007 US.P. P. CURRENT APPLICATION NUMBER: US/10/408,736 CURRENT FILING DATE: 1999-08-23 PRIOR APPLICATION NUMBER: US/09/379,095A PRIOR PILING DATE: 1999-08-23 PRIOR PILING DATE: 1999-09-02 NUMBER OF SEQ ID NOS: 81 SOFTWARE FALSEQ for Windows Vermion 4.0 SEQ ID NO 56 LENGTH: 278
                                                                                                                                                                                                                                                                                           Sequence 56, Application US/10408736
Publication No. US20030177508A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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Das, Tapas
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Best Local
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RESULT B

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FILE REFERENCE: 21402-157

TITLE OP INVENTION: No. US20030190715Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-157

CURRENT APPLICATION NUMBER: US/09/976,782

CURRENT FILING DATE: 2000-10-12

PRIOR APPLICATION NUMBER: 60/240,113

PRIOR APPLICATION NUMBER: 60/240,662

PRIOR FILING DATE: 2000-10-16

PRIOR FILING DATE: 2000-10-16

PRIOR FILING DATE: 2000-10-16

PRIOR FILING DATE: 2000-10-16

PRIOR PILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,732

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,732

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,703

PRIOR PILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,703

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: 60/240,703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 RSLYABGFYKTLCYSCNPTD-VAAFWSFAPALSKIVELGDTMPIILRKRPLIFLHYYHHA 167
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41.6%; Pred. No. 2e-41;
tive 47; Mismatches 87; Indels
                                                                               GENERAL INFOGRATION:
GENERAL LINCORDAL LOW:
APPLICANT: Abbott Laboratories
APPLICANT: Laborard, Amanda Eun-Yeong
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng,
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER: OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S: LENGTH: 271
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Publication No. US20030190715A1
GENERAL INFORMATION:
Sequence 53, Application US/09903456 Patent No. US20020138874A1 GENERAL INFORMATION:
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Best Local Similarity 41.69
Matches 101; Conservative
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US-09-903-456-53
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151

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49 OKYWYHSITISVLYFILIKVIQKFMENRKPPTLKYPLILMNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                                      168 AVLIYTVHSGABHTAAGRFYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQM 227
                                                                                                                                                                                                                               212 VLGTIFGILNYIMR----QEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRPKGKVA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 RSLYARGFYKTLCYSCNPTD-VAAFWSFAFALSKIVELGDTMFIILRKRPLIFTLHYYHHA 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 OKYWYHSITISYLYFILIKYIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL
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                                                                                                                               109 RSLYARGFYKTLCYSCNPTD-VAAFWSPAFALSKIVELGDTMFIILRKRPLIFLHYYHHA
                                                                             32 BEYWYSSFLIVVVYILLIVVGQTYMRTRKSFSLQRPLILWSFFLAIFSILGTLRMWKFWA
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                  Gaps
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31.0%; Score 479; DB 14; Length 271;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 97; Indels
; Pred. No. 2e-41; 47; Mismatches 87; Indels
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Matches 101; Conservative 4
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; ORGANISM: Mus muculus
US-10-408-736-50
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6070.US.P4
CURRENT APPLICATION NUMBER: US/10/156,911
CURRENT RILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-01
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 12000-07-24
PRIOR FILING DATE: 1909-08-23
PRIOR FILING DATE: 1909-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FSELSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.0%; Score 479;
PRIOR FILING DATE: 2000-10-16
PRIOR PAPPLICATION NUMBER: 60/240,637
PRIOR PILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/240,669
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR APPLICATION NUMBER: 60/240,648
PRIOR PILING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 127
SEQ ID NO 107
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/10156911
, Publication No. US20030163845A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 41.6%;
Matches 101; Conservative 4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-10-156-911-53
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
US-09-976-782-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKS 287
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US-10-156-911-53
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TYPE: PRT
ORGANISM: Mus musculus
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NAME/KEY: VARIANT
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31.0%; Score 479; DB 9; Length 272;
Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels
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COCATION: (272)...(272);
OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24
                                                                                                                                                                       APPLICANT: Mukerii, Fradip
APPLICANT: Honard, Amanda Run-Yeong
APPLICANT: Heonard, Amanda Run-Yeong
APPLICANT: Heonard, Amanda Run-Yeong
APPLICANT: Hereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
TILE REPERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1939-08-03
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1939-08-03
PRIOR FILING DATE: 1938-09-02
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/10156911
Sequence 24, Application US/10156911
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hendry, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Pereira, Suzette L.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P4
                                                                                               Sequence 24, Application US/09903456
Patent No. US20020138974A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
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268 SKS 270
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CTREARY APPLICATION NAMES: US 09/903-456
PRIOR PLING DATE: 2001-10-711
PRIOR APPLICATION NAMES: US 09/903-456
PRIOR PLING DATE: 3000-10-711
PRIOR APPLICATION NAMES: US 09/903-456
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Search completed: June 16, 2004, 15:34:59
Job time : 49 secs
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                                                                                                                                                                                                                                                                                     109 RSLYAEGFYKTLCYSCNPTD-VAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHHA 167
                                                                                                                                                                                                                                                                                                                  92 TWAFTVGLKQTVCFAIYTDDAVVRFWSFLFELSKVVELGDTAFILLRKRPLIFVHWYHHS 151
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                                                                                                                                                                                                  49 OKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL 108
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                                                                                                                                                                                                                        32 EEYWVSSFLIVVVYLLLIVVGGTYMRTRKSPSLQRPLILMSPPLAIFSILGTLRWMKFWA 91
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Best Local Similarity 40.2%; Pred. No. 3.4e-41;
Matches 99; Conservative 49; Mismatches 87; Indels 11; Gaps
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Best Local Similarity 41.6%; Pred. No. 2e-41;
Matches 101; Conservative 47; Mismatches 87; Indels
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LOCATION: (218)...(218)
CTHER INFORMATION: Xaa = Unknown or Other at position 218
US-09-903-456-60
NAME/KEY: VARIANT
COCATION: (272)
COTHER INFORMATION: Xea = Unknown or Other at position 272
US-10-408-736-21
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APPLICANT: Mukerji, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Henny Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US: P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1999-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PSESEE OF Windows Version 4.0
SEQ ID NO 66
SEQ ID NO 66
SEQ ID NO 66
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, Sequence 60, Application US/09903456

; Patent No. US20020138874A1

; GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
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SKS 270
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73 APELIHVLRHYGLPHSVCVPSYIEQDRVCGFWTWLFVLSKLPELGDTIPIVLRKQPLIFL 132
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1545
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	protein C40E rr-1993 #sequence to the EvBL Dat the EvBL Dat tumber: S2829 \$28299 \$28299 \$28299 \$28299 \$28299 \$28290 \$2291 <ber> cences: EwBL></ber>	al protein [Ceanorhabdi - Oct. 1999 #s n: T34200 Gattung, S. to the EMBL Lion: The sec
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A; Map position: 4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Cocession: T20786
R;Matthews, L.
Submitted to the EMBi Data Library, October 1996
A;Accession: T20786
A;Accession: 279786
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Coss-references: EMBL:Z81058; pIDN:CAB02921.1; GSPDB:GN00022; CESP:F11E6.5
A;Experimental source: clone F11E6
C;Gentics:
A;Gentics:
A;Gentics:
A;Map position:
A;Introns: 38/3; 99/1; 183/2; 235/2
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A,Accession: T34200
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 1-435 < 60052>
A,Cross-references: EMBL:U41011; PIDN:AAA82288.1; CESP:D2024.3
A,Gene: CESP:D2024.3
A,Introns: 17/3; 306/1; 398/3
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, Pred. No. 1.2e-27;
48; Mismatches 99; Indels
                                                                                                                                                                               86; Indels
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36.5%; Score 564; DB 2;
Best Local Similarity 42.0%; Pred. No. 4.9e-42;
Matches 128; Conservative 45; Mismatches 86
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procein P41H10.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88690
R;anonymous, The C elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biold A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biold A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a. A;Accession: H88690
A;Accession: H88690
A;Residues: 1-274 <STO>
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C;Genetics:
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Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: T2-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 17-Mar-2000
Cidcession: T2-189
Riwilkinson, J.
Submitted to the EMBL Data Library, January 1996
Airefarence number: Z19616
Airefarence number: Z19616
Airefartus: preliminary; translated from GB/EMBL/DDBJ
Airefartus: preliminary; translated from GB/EMBL/DDBJ
Airefartus: DNA
Airefartus: EMBL: Z68749; PIDN: CAA92958.1; GSPDB: GN00022; CESP: F56H11.4
Airefartus: CESP: F56H11.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 KIVELGDIMPIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYPAHSLMYT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVAN----LY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
   291
                                   216 IPGHLVFIKSADSVPGCAVŠMAVLSIGGLMYISYLFLFAKFFXKAYIQKKS-PTKTSKQE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYABGFYKTLCYSCN-PTDVAAFWSFAFALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 BVLTTAPPSHELSKKHIAQTQY-----AAFW-----ISMAYVVIPGLKAVMTNRKPFDL
233 ITWMVYKYKTBYKLP-CQQSVANLYLAFVIYVTPAILFIQFFVKAYIIKSSKKSKKNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 DMTTKYKYSYHFPGEQVADPQYWILLFQKYWYHSITISVLYFILLKVIQKFMENRKPFTL
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A;Gene: CBSP:P56H11.4
A;Map position:
A;Introns: 49/3; 110/1; 238/3
C;Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

24.2%; Score 374; DB 2; Length 27

Best Local Similarity 30.4%; Pred. No. 1.6e-25;

Matches 83; Conservative 59; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 LAFVIYVTFALLFIQFFVKAYIIKSSKKSKSVK 289
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Caenorhabditis elegans

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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22791
R;Wilkinson, J.
S;Wilkinson, J.
S;W
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                                                                                                                                                                                                                                                      108 LRSLYAEGFYKTLCYSCNPT-DVAAFWSFAFALSKIVELGDTWFIILRKRPLIFLHYYHH 166
                                                                                                                                                                                                                                                                                           167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                               160 ILFWIYAWYSHPLTPGFNRYGIYLNFVVHAFMYSYYFLRSMKIRVPGPIAQAITSLQIVQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 MLAGVGITWRVYKVKTEYKLPÇQQSVANLYLAFVIYVTFAILFIQPFVKAYIIKSSK-KS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAA92960.1; GSPDB:GN00022; CESP:F56H11.3
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BLWSLLTNQDEVFPHIRARRIQEHFGLFVQMAIAYVILVFSIKRFMRDREPFQLTTALR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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                                                                                                                                                                                         PADHEDVIIQASILYMVVVPGTKWFWRNRQPFQLIIPLNIWNFILAAFSIAGAVKMIPEF
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   Length 288,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93; Indels
23.3%; Score 360; DB 2; Length 28 31.3%; Pred. No. 2.9e-24; ive 58; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 329; DB 2;
; Pred. No. 1.5e-21;
49; Mismatches 93;
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E88650
protein P41H10.7 [imported] - Caenorhabditis elegans
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Best Local Similarity 31.7%;
Matches 77; Conservative 4
Query Match
Best Local Similarity 31.34
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282
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Cipter: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 Cipter: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 Ciptecession: E88690 #sequence_revision 10-May-2001 Ciptecession: E88690 #NID: 99069613; PMID: 9851916 A; Mitter: Genome sequence of the nematode C. elegans: a platform for investigating biolo A; Mitter: Genome sequence of the nematode C. elegans: a platform for investigating biolo A; Mitter: See websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A; Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A; Mitters: preliminary A; Mitters: preliminary A; Mitters: 1-286 <STO> A; Mitters: 1-286 <STO> A; Mitters: 1-286 <STO> A; Mitters: Testerences: GB:chr_IV; PIDN:AAB03174.1; PID:g1397335; GSPDB:GN00022; CESP:F41H1
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: T3734; T39101
R;Wedler: H; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VAIFAQVHVSYKHYVEGVEGLAYSFRGTAIGFFMLTTYFYLMIQFYKEHYLKNGGKKYNL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRS-LYA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 AGV-GITWMYYKVKTEYKLPCQQSVANLYLAPVIYVTFALLPIQPFVKAYIIKSSKKSKS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YTV----HSGAEHTAAGREYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQML
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A,Introns: 5/2; 125/3
C,Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 327.5; DB 2; Length 32.8%; Pred. No. 2.1e-21; ive 44; Mismatches 109; Indels
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A;Molecule type: DNA
A;Residues: 1-328 <WED>
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A;Molecule type: DNA
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Hes 80; Conserv
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A, Map position: 4
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Best Local S:
Matches 80
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GSPDB:GN00066; SPDB:SPAC1B2.03c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 IDPLRSLYAEGFYKTLCYSCNPTDVAAFWSFAFALSKIVELGDIMFIILRKRPLIFLHYY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNSI/SUR4 family protein [imported] - fission yeast (Schizosaccharomyces por Cispecies: Schizosaccharomyces pombe Cispecies: Schizosaccharomyces pombe Cibate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 CiAccession: TS0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 YKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILLIKVIQKFME--NRKPFTLKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 VELGDIMFIILRKRPLIFLHYYHH--AAVLIYTVHSGAEHTAAGRPYILMNYFAHSLMYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 FEYFSGYPAEQPEFIHNKTPLAN--GYHAVSIIIVYYIIIPGGQAILRALNASPLKFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 LILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLC--YSCNPTDVAAFWSFAPALSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 YYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTEY-------KLPÇQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 YHSITISV-LYFILIKVIQKFMENRKP-----FTL-KYPLILWNGALAAPSIIATLRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HH - - AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTTVSAMGYRLPKWYSMTVTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 345;
                                                                         A.Map position: 12R
C;Superfamily: Saccharomyces probable membrane protein YCR034w
C;Keywords: transmembrane protein
F;69-89/Domain: transmembrane #status predicted <TM1>
F;140-129/Domain: transmembrane #status predicted <TM2>
F;148-166/Domain: transmembrane #status predicted <TM3>
F;209-229/Domain: transmembrane #status predicted <TM4>
F;283-263/Domain: transmembrane #status predicted <TM6>
F;283-304/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.0%; Score 262; DB 2; Length 349
28.9%; Pred, No. 1.5e-15;
ive 53; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 GTQAAAYGYLILTSYLLLFISFYIQSY----KKGGKKTVKKE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 QSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKK--SKSVKNE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 235.5; DB 2; 28.2%; Pred. No. 3.1e-13; iive 50; Mismatches 102;
    A;Gene: SGD:SUR4; SRB1; APA1
A;Cross-references: SGD:S0004364; MIPS:YLR372w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.2<sup>3</sup>
Matches 71, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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ses 82, Conserve
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Best Local S:
Matches 82
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Ribu, 20

Ribu, 20

Ribu, 20

Ribuscription: The sequence of S. cerevisiae cosmid 8039.

A; Reference number: $51377

A; Accession: $51377

A; Recent contains to the State of S. Cerevisiae cosmid 8039.

A; Reference since in the State of S. Cerevisiae cosmid 8039.

A; Rocession: $51377

A; References: EMBL: U19103; NID:g609404; PID:g609406; MIPS:YLR372w

A; Rolacule type: DNA

A; References: EMBL: U19103; NID:g409404; PID:g609406; MIPS:YLR372w

B; Garcia-Arranz, M.; Maldonado, A.M.; Mazon, M.J.; Portillo, F.

A; Reference number: A54902; MUID:94299524; PMID:8027068

A; Reference number: A54902; MUID:94599524; PMID:GA55129-1; PID:g467698

A; Residues: 1-34, 'D', 36-207, 'R', 208-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: 1-34, 'D', 36-207, 'R', 201-329, 'PY', 332-345 cGAR>

A; Residues: Distance of sequence not shown

A; Residues: 1-345 cREW>

B; Residues: 1-345 cREW>

B; Residues: 1-345 cREW>

A; Residues: 1-345 cREW>

B; Residues: 1-345 cREW>

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A;Reference number: 348517
A;Accession: $48517
A;Accession: $48238
A;Besidues: 1-345 <REU>
A;Cross-references: EMBL:L28723; NID:g453567; PID:g453568
A;Cross-references: EMBL:L28723; NID:g453567; PID:g453568
A;Cross-references: EMBL:Data Library, October 1994
A;Description: Sterol isomerase is a target for the immunosuppressant SR 31747 in saccha A;Accession: $48238
A;Accession: $48238
A;Accession: $48238
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N;Alternate names: protein L8039.2; protein YLR372w; regulatory protein APA1; SRE1 prote
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: S48517; S48238; S51390; A54902; S59600; S43122; S49468
R;Revardel, E.
                                                                                                                                                                                                                                                                                                                                                                            FPSICNEKAWTQPLVFLYYCAYISKFLELTDTPFLVLRKKPLQFLHCYHHGATAVLVYTQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 TISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAPSIIATLRFSIDPLRSLYAEGF 116
                                                                                                                                                                                                                                                                                                                            117 YKTLCYSCNPTDVAAFWSPAFALSKIVELGDTMPIILRKRPLIFILHYYHH--AAVLIYTV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSGAEHTAAGREYILMNYFAHSLMYTYYTVSAMGYRLP--KWVSMTVTTVQTTQMLAGVG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 IVG--RTSISWLIIEINLLVHVTWYYYYYLVAKGIRVPWKKW----VTRPQIVQFPADLG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITWMVYKVKTEYKLP-----CQQSVANLYLAFVIYVTPAILFIQFFVXAYIIKSSKK 284
                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                    Gaps
                                                                                  23;
             Length 328;
    th 18.2%; Score 281.5; DB 2; Length Similarity 31.0%; Pred. No. 2.7e-17; 76; Conservative 36; Mismatches 110; Indels
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R;Du, Z.
Query Match
Best Local Similarity
Matches 76; Conserv
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A,Accession: S1216
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-347 < THIL.
A,Cross-references: 1-347 < THIL.
A,Cross-references: BNBL:X56909, NID:94489, PIDN:CAA40226.1; PID:94490
B,Wicksteed, B.L.; Roberts, A.B.; Sagliocco, P.A.; Brown, A.J.P.
R,Wicksteed, B.L.; Roberts, A.B.; Sagliocco, P.A.; Brown, A.J.P.
A,Title: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces A,Reference number: S40917; MUID:92133166; PMID:1776366
A,Accession: S40919
                                                                                       chromosome III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 YYVIİFGERFLISKSKPFKLNGLFÇLHNIVLISLSLILLLIMVEQLVPIIVQHGLYFAIC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 YSCNPTDVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH -- AAVLIYTVHSGAE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 -TSISWVPISLNLGVHVVVMYWYYPLAARGIRV--WWKGWVTRFQIIQFVLDIGFIYPAVY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 HTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVG-ITWWVY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 KVKTEYKLP-----CQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVK 289
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R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross references: EMBL:S78624; NID:g244237; PIDN:AAB21260.1; PID:g244240
R;Dujon, B.; Pairhead, C.; Thierry, A.
submitted to the Protein Sequence Database, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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R;Thierry, A.; Fairhead, C.; Dujon, B.
Yeast 6, 521-554, 1990
A;Title: The complete sequence of the 8.2 kb segment left of MAT on
A;Reference number: S12916; MUID:91181345; PMID:1964349
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C;Date: 04-Feb-2000 #sequence revision 04-Feb-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 3R
C,Superfamily: Saccharomyces probable membrane protein YCR034w
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A;Molecule type: mRNA
A;Residues: 1-158 <AAA>
A;Cross-references: EMBL:AL137506
A;Experimental source: adult amygdala; clone DXF2p7610031
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKeywords: transmembrane protein
F)67-84/Domain: transmembrane #status predicted <TM1>
F)110-129/Domain: transmembrane #status predicted <TM2>
F)153-169/Domain: transmembrane #status predicted <TM3>
F)198-214/Domain: transmembrane #status predicted <TM3>
F)236-254/Domain: transmembrane #status predicted <TM4>
F)275-299/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp7610031.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: SGD:S0000630; MIPS:YCR034w
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A, Reference number: Z23031
A, Accession: T46257
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A; Residues: 1-347 < DUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
A, Residues: 1-347 <WIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S19446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YCR034w homolog YJL196c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J0343; protein YJL196c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S46638; S56983
R;Purnella, B; Coster, F; Goffeau, A.
R;Purnella, B; Coster, F; Goffeau, A.
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifie as gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46631; MUID:95274326; PMID:7754713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : : : | | | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                      QTTQMLAGVGITWMVYKVKTEYK----LP----CQQSVANLYLAFVIYVTFAILFIQFFV 274
                                                                                                               224 QIIQPVLDLILCYFGTYSHIAFRYPWLPHVGDCSGSLFAAFFGCGVLSSYLFLFIGFYI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LYPILIKVIQKPMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTL 120
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A,Status: nucleic acid sequence not shown
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNA
B,Cross-references: EMBL:X77688; NID:g1183992; PIDN:CAA54764.1; PID:g547599
R;Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein_Sequence Database, September 1995
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N;Alternate names: hypothetical protein YCR521
C;Species: Saccharomyces cerevisiae
C;Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 21-Jul-2000
C;Accession: S12916; 640199; S19446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-310 <PUW>
A;Cross-references: EMBL:249471; NID:g1008410; PID:g1008411; MIPS:XJL196c
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C;Superfamily: Saccharomyces probable membrane protein YCR034w
C;Keywords: transmembrane protein
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Similarity 27.0%; Pred. No. 5.9e-12;
66; Conservative '48; Mismatches 111;
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A;Cross-references: SGD:S0003732; MIPS:YJL196c
                                                                                                                                                                                                                          275 KAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                 284 NTYÍKRGAKKNO 295
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Best Local Simi
Matches 66;
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Fer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                         A; Accession: D96693
A; Ataus: preliminary
A; Molecule type: DNA
A; Residues: 1-1435 <STO>
A; Cross-references: GB: AE005173; NID: g9755445; PIDN: AAF98206.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A,Gene: Putative ABC transporter
A,Gene: Putative ABC transporter
A,Map position: 1
C,Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
          408, 816-820, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: clone Y47D3A
C;Genetics:
A;Gene: CESP:Y47D3A.14
A;Introns: 17/2; 51/3; 102/3; 169/3; 246/1; 287/2; 319/3; 371/3; 395/2; 440/3; 450/3;
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                                                                                                                                                                                                                                    141 KIVELGDTMFIILRKR--PLIFIHYYHHAAVLIYTVHSGAEHTAA--GRFYILMNYFAHS 196
                                                                                                                                                                                                                                                                                                                                                                                                                   60 VMYSYYGLSALGPAYQXYLWWKKYLTSLQLVQFVIVALHISQPFFMEDCKYQPPVPACII 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFNFRPSHISDRSY---LKEWYXYNCVFQLGLGILMI------PEILTSSLSGWH 523
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                                                                                                                                                                                                                                                                            30 SYHFPGEQVADPQYWT1LFQKYWYHSITISVLYFILIKVIQKFMENRKFFTLKYPLILEWN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Caenorhabditis elegans
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                                                                                                         Length 158;
A;Note: DKFZp7610031.1
C;Superfamily: Saccharomyces probable membrane protein YCR034w
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVKN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y47D3A.14 - Caenorhabditis elegans
                                                                                                  , DB 2;
1.1e-09;
                                                                                                  12.4%; Score 191; DB
llarity 31.8%; Pred. No. 1.1e
Conservative 36; Mismatches
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Best Local Similarity
Matches 57; Conserv
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50; Conserv
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                                                                                                     Query Match
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cassette homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1294 LWFYYYMLTSFIYFTLYGMMLMALTPNYQIAGICMSFFLSLWNLFSGFLIPRPQIPIWWR 1353
                                                                                                                                                                                                                                                                                                    55 --SITISYLYFILIKVIQKFMENRKP----FTLKYPLILWNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 IFLHYYHHAAVLIYTVHS-----GAEHTAAG----RFYILMNYFAHSLM-----Y 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 TYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYK-----LPCQQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                           RSLY----AEGFYKTLCYSCNPTDVAAFWS-----FAFALSKIVELGDTMFIILRKRPL
                                                                                                                                                                                5 SEWNDINTFILYGPNHIDMTIKYKYSYHFPGEQVAD--PQYWIILFQKYMYH-----
                                                                                                                          Gaps
                                                                                                                       87;
                                                                                                                       Indels
                                                         7.6%; Score 117.5; DB 2;
21.8%; Pred. No. 0.037;
trive 55; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 SVANLYLAFVIYVTFAILFIQFFVKAYIIK 280
                                                         Query Match
Best Local Similarity 21.8<sup>†</sup>
Matches 72, Conservative
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completed: June 16, 2004, 15:29:33

Q81273 plasmodum Q91174 chizosacch Q9b1r0 leishmania Q7ztu5 brachydanio Q8fip4 dictyosteli Q8m802 drosophila Q9th7 drosophila Q9th7 drosophila Q7zuc3 brachydanio Q7zuc3 brachydanio

Q8i251 plasmodium Q7zxj4 xenopus lae

Q8jzv3 mus musculu Q8jzv3 mus musculu Q8avg1 xenopus lae Q7sv10 brachydanio Q9vh56 drosophila Q8byy8 mus musculu Q9j5f5 fowlpox vir Q9dzy9 mus musculu Q8dzy9 mus musculu Q8dzy9 mus musculu Q8dzy9 mus musculu

09gnx8 leishmania 09bhq9 leishmania 09vh59 drosophila 09vcz0 drosophila 08wxu3 homo sapien 08ut7 schizosacch 09utf7 schizosacch

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2 BLABFWNDINTFTIYGPNHTDMTTKYKYSYHFPGRQVADPQYWTIL-----FQKYWYHSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.7%; Score 659.5; DB 5; Length 286; Best Local Similarity 45.1%; Pred. No. 2.4e-50; Matches 130; Conservative 51; Mismatches 88; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for investigating biology", "Investigating biology", "Science 263:2012-2018 (1998).

EMBL, AL132949; CAB61069.1; -...
WornPep; 793781-3; GE22388.

GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IPR002076; GNSI_SUR4.

PROSITE; PR01151; ELO; 1.

PROSITE; PR01151; ELO; 1.

PROSITE; PR01168; ELO; 1.

SEQUENCE 286 AA; 33402 MW; DF9DB8D3B2PIC479 CRC64;
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.4e-50;
.aa 88; Indels
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Last sequence update)
Last annotation update)
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                                                    Q9UR34
Q9BLR0
Q7ZTUS
                                                                                                           Q86HP4
Q8MS02
Q94IPL8
Q9VHX7
Q7ZUC3
Q9VN29
Q8JZV3
Q8JZV3
Q7SY74
Q7SY74
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Q9J5F5
Q9D2Y9
Q8BX38
  Q81251
Q72XJ4
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09VH59
09VCZ0
08WXU3
0871S5
090TF7
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MEDLINE=99069613; PubMed=9851916;
  01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24, X53F4B.2 protein.
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315

2833.5 5 2835.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2335.5 5 2355.5 5 2355.5 5 2355.5 5 2355.5 5 2355.5 5 2355.5 5 2355.5 
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Q802x6 brachydanio
Q92016 rattus norv
Q80c45 mus musculu
Q9h5j4 homo sapien
Q8ncd1 homo sapien
Q8ncd1 homo sapien
                                                                                                                   June 16, 2004, 15:24:53; Search time 45 Seconds (without alignments) 2040.351 Million cell updates/sec
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Ogvv87 drosophila
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caenorhabdi
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caenorhabdi
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1 MELAEFWNDLNTFTIYGPNH......PPVKAYIIKSSKKSKSVKNE 291
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Q9VW87
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sp_rodent;*
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                                                                                                                                                117 YKTLCYSCNPTDVAAFWSFARSKIVELGDTMFILLRKRPLIFLHYYHHAAVLIYTVHS 176
                                                                                                                                                                                                                                                                                  177 GAEHTAAGRFYILANYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWM 236
                        TISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGF 116
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MEDLINE=20196006; PubMed=10731132;
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Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Barans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
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Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
Perriera S., Prise B., Galle R.P., Garg N.S., George R.A.,
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Lybmitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
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C Stantament C. Dorset V., Ragbayani A., Carlson J.,

C Stantament C. Dorset V., Faise B., George R.,

Champe M., Chavez C., Dorset V., Faise B., George R.,

Conzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

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A Yu C., Lewis S.E., Raubin G.M., Celniker S.,

B. Submitted (OCT-2001) to the EMBL/GenBank/DDEJ databases.

B. Submitted (OCT-2001) to the EMBL/GenBank/DDEJ databases.

BR MBL; ARE03526; AAF5771.1; -.

BR REBL; ARE03526; AAF5771.1; -.

BR REBL; ARE03526; AAF602080.1; JOINED.

BR REBL; ARE03526; AAF602080.1; JOINED.

BR PREL; ARC001121; AAL28669.1; -.

BR GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

BR CO; GO:0006118; P:oxidoreductase activity; IEA.

BR InterPro; IPR05206; Rieske_dom.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 AA; 36829 MW; B741960F28D2A3AD CRC64;
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Science 287:2185-2195 [2000].
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PROSITE; PS01188; ELO; 1.
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184 RAAGPRUSRKFAMFITLSQITQMLMGCVINYLVPNWMQHDNDQCYSHFQNIFWSSLMYLS 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LGDTIFIILRKQKLIFLHWYHHITVLLYSWYSYKDXVAGGGWFWTMNYGVHAVMYSYYAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 SAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                    LGDTWFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTV
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                                                                                                                                                                                                                                                                      26 KYKYSYHPPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
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01-070-2003 (TrEMBLIEL) 25, Last sequence update)
01-070-2003 (TrEMBLIEL) 25, Last annotation update)
01-077-2003 (TrEMBLIEL) 25, Last an
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                    DB 11; Length 267;
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                                                                                                                                       29.0%; Score 44.00; 36.9%; Pred. No. 1.2e-31; 106:18 ive 50; Mismatches 109; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Strausberg R.; Submitted (FRB-2003) to the EMBL/GenBank/DDBJ databases. Submitted (FRB-2003) AAH46501.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0016021; C:integral to membrane; IEA. FR00202076; GNS1_SUR4. FR00151; ELO; 1.
                                                                                       4026C9CB33FDDD23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 AA; 31386 MW; CDD41ACA11639928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 447; DB 13; 36.2%; Pred. No. 1.4e-31; tive 60; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 PAILFIQFFVKAYIIKSSKKSKS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 YLVLFCHFFFEAYIGKVKKATKA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
InterPro; IPR002076; GNS1_SUR4
                                                                                    31610 MW;
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nes 101, Conservative
                                                                                                                                                                                                               97; Conservative
                                                          ELO; 1
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                         Pfam; PF01151; ELO;
PROSITE; PS01188; El
SEQUENCE 267 AA;
                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
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                                                                                                                                                                                                                                                                                                         60 PRPQLRGPLIMNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIZQDRVCGFWT 119
                                                                                                                                                                                                                                                                                                                                                                                                                       77 KPFTLKYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGPYKTLCYS--CNFTDVAAFWS 134
                                                                                                                                                                                                                                                                                                                                                                                          FAFALSKIVELGDIMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQMLAGVGI-TWMVYKVKTBYKLPCQQSVA 253
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                                                                                                                                                                                                     VIPNYSYIFDFENDFIHQRIRKMMLENWIWVF---YYCGI----YMLVIFGGGHEWQNR 59
                                                                                                                                                 23 MITKYKYSYHFPGEQVADP-----QYWTILFQKYWYHSITISVLYFILIKVIQKFMENR
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fatty acyl elongase (Long-chain fatty-acyl elongase) (Myelination associated SUR4-like protein).
BLOVIG OR FAE OR LCE OR MASR.
Mus musculus (Mouse)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7B16; TISSUB=Liver; Matsuzaka T., Shimano H.; Matsuzaka T., Shimano H.; murine complete cds for new fatty acyl elongase similar to cig30 (197107).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE=21576178; PubMed=11567032; Marrington J.A., Horton J.D.; Moon Y.A., Shah N.A., Mohapatra S., Warrington J.A., Horton J.D.; Identification of a Mammalian Long Chain Fatty Acyl Elongase Regulated by Sterol Regulatory Element-binding Proteins."; J. Biol. Chem. 276:45358-45366 (2001).
                                                                                       17;
                             Length 316;
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Nagarajan R., Le N.H., Mahoney H., Araki T., Milbrandt J.D.,
"Deciphering Peripheral Nerve Myelination Using Schwann Cell
Expression Profiling.",
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                       Indels
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                      31.4%; Score 484.5; DB 5; 37.7%; Pred. No. 7.9e-35; ive 54; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 NLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 NINLSIAMYSSYFVLFARFFYKAYLAPGGHKSR 272
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STRAIN-CZECH II; TISSUE-Breast tumor;
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                       Similarity
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                                                                             103;
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                      Query Match
Best Local S
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244 YLVLFCHFFFEAYIGKVKATKA 266
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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Best Local S:
Matches 96
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Q9H5J4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCDIMPIILEKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYYTV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGDTIPIILRKQKLIPLHWYHHITVLLYSWYSYKDMVAGGWFWTMNYGVHAVMYSYYAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 SAMGYRLEKWVSMTVTTVQTTQMLAGVGITWMVYKVKTEYKLECQQSVANLYLAFVIYVT 264
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STRAIN=Sprague Dawley; TISSUE=Liver;

A Inagaki K., Aki T., Pukuda Y., Kawamoto S., Shigeta S., Ono K.,

A surathi O.;

"Identification and expression of a mammalian fatty acid elongase involved in de novo biosynchesis of C18 fatty acids.";

Tuvolved in de novo biosynchesis of C18 fatty acids.";

EMBL; ABOT1986; BAB6988.1; -.

GO: GO:0016021; C:integral to membrane; IEA.

R interPro: IPRO2070; ONSI_SUR4.

R Pfam: PF01151; ELO: 1.

R PROSITE; PS01188; ELO: 1.

R PROSITE; PS01188; ELO: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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BLOVL6 OR LCB.
Mus musculus (Mouse).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mus. Musi TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Mismatches 109; Indels
                                                                      232 DNIVWASLMYLSYLLLFSSFFYQSYM--KSSKPESIKRE 268
                             253 ANLYLAFVIYVTFAILFIQFFVKAYIIKSSKKSKSVKNE 291
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01-XAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Long chain fatty acyl elongase.
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Last annotation update)
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Skin;

TABLINE=23454683, PubMed=12466851;

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A thalysis of the mouse transcriptome based on functional annotation of a consortium, by the RIKEN Genome Exploration Research Group Phase I & II Team;

Thalysis of the mouse transcriptome based on functional annotation of the G0,770 full-length cDNAs.";

Nature 420:563-573 (2002).

REMBI, AKC92029; BAC26522.1; ...

ROD: MOI:2156528; Elovie.

ROD: MOI:2156528; Elovie.

ROD: G0:0030176; Cintegral to endoplasmic reticulum membrane; IDA.

ROS: G0:0030497; P:transferase activity, transferring groups o. .; IDA.

ROS: G0:0030497; P:fatty acid elongation; IDA.

ROS: G0:0030497; B:fatty acid elongation; IDA.

ROS: G0:0030497; B:fatty acid elongation; IDA.

ROS: G0:00151; ELO: 1.

ROD: ROS: G0:0030497; RIM: 4031P9C503B4DD23 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 RAAGFRUSKKFAMFITLSQITÇMLMGCVINYLVFNWMQHDNDQCYSHFQNIFWSSLMYLS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 LGDTMFIILRKRPLIFLHYYHHAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 SAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPÇQQSVANLYLAFVIYVT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 ILWNGALAAFSIIATLRFSIDPLRSLYAEGPYKTLC-YSCNPTDVAAFWSFAFALSKIVE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 SYEPEKOFNENBAIO---W---MOENWKKSFLFSALYAAFIFGGRHLMNKRAKFELRKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 KYKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto & Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogano S.;

Tanaka T., Nakamura Y., Isogano S.;

"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 28.4%; Score 439.5; DB 11; Length Local Similarity 36.5%; Pred. No. 6.3e-31; Lengthes 96; Conservative 50; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027031; BABL563.1; -.
Genew; HGNC:15829; ELOVIG.
GO; GO:0016021; C:integral to membrane; IEA.
Interprey; IPR002076; GNS1_SUR4.
PFam; PF01151; ELO; 1.
PROSITE; PS01188; ELO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein FLJ23378.
Homo sapiens (Human)
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96 GFVASYCQNENYYTDASTGFWGWAFVWSKAPBLGDTWFLVLRKKKPVIFWHHHALTFVY 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 ITWWYKVKTEYKLP-CQQSVANLYLAFVIYYTFAILFIQFFVKAYIIKSSKKSKKVKE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 IFGHLVFIKSADSVPGCAVSMNVLSIGGLAYISYLPLFAKFFYKAVIQKRS-PTKTSKQE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 SITISVLYFILIKVIQKFMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRSLYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 GPYKTLCYSCN-PIDVA-AFWSFAPALSKIVELGDTWFIILRKRPLIFLHYYHHAAVLIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 AVVIYSEHQAWARWSLALMLAVHIVMYFYPAVRALNIQIPRPVAKFITIIQIVQFVISCY
                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.8%; Score 398; DB 5; Length 27 37.1%; Pred. No. 3e-27; ive 48; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptosporidium parvum.
Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimerlida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WormPep; F1186.5; CE19785.

GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPRO02076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
SEQUENCE 274 AA; 31361 MW; 2CBB7DASF418D714 CRC64;
                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative fatty-acyl elongase.
                                                                                                                                                            274 AA
                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281058; CABO2921.1; --
PIR; T20786; T20786.
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                                                                                                                                                                                                                                                          Caenorhabditis elegans.
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nes 89; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                              F11E6.5 protein.
F11E6.5.
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238 KA 239
                                                           286 KS 287
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                                                                                                                                                         142
                                                                                                                                                                       109 RSLYAEGFYKTLC---YSCNPTDVAAFWSFAFALSKIVBLGDTWFIILRKRPLIFLHYYH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 YILMTKGLKQSVCDQGFYNGP--VSKFWAYAFVLSKAPELGDTIFIILRKQKLIFLHWYH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLFKWVSMTVTTVQTT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                 :|::
EYEFEKQFWENEALQ---W----MGENWKKSFLFSALYAARIFGGRHIMNKAKFELRKPL
                                                                                                                                                      86 ILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLC---YSCNPTDVAAFWSFAFALSKI
                                                                                             26 KYKYSYHPPGEQVADPQYWTILFQKYWYHSITISVLYFILLKVIQKFWENRKPFTLKYPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      13;
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                                           DB 4; Length 265;
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                                      / Match 28.2%; Score 435.5; DB 4; Length; Local Similarity 35.8%; Pred. No. 1.4e-30; nes 95; Conservative 54; Mismatches 103; Indels
 l protein.
265 AA; 31376 MW; 01234E0EEF6CE341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 AA
                                                                                                                                                                                                                                                                                                                         263 VTFALLFLOFFVKAYIIKSSKKSKS 287
                                                                                                                                                                                                                                                                                                                                           240 LSYLVLFCHFFFEAYIGKMRKTTKA 264
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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nes 92; Conservative
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Hypothetical
SEQUENCE 26
                                        Query Match
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                                                                   Matches
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9

qc ò g ò 9

Gaps

20;

Length 274;

DDF0840C1454A4CD CRC64;

membrane; IEA

140

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180 YYMLRSFGVKVPAMIAKNITTMQILQFV----ITHFIL-FHVGYLAVTGQSVDSTFGYYW 234
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                                                                                                                                                                                                                                                                                                                              82 KYPLILWNGALAAFSIIATLRFSIDPLRSLYAEGFYKTLCYSCN-PTDVAAFWSFAFALS
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                                                                                                                                                                                                                                                                                               22 DMTTKYKYSYHPPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTL
                                                                                                                                                                                                    Query Match

24.2%; Score 374; DB 5; Length 27
Best Local Similarity 30.4%; Pred. No. 4e-25;
Matches 83; Conservative 59; Mismatches 111; Indels
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01-MAR-2001
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 TVSAMGYRLPKWVSMTVTTVQTTQMLAGVGIT--WMVXKVK-----TBY----KLP 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 YLSSCGKR-PKW-GMIITILQIVQMIIGTILTTSGMYYSYKHPFANVFPVBYLSQPLKVG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 KYLTLPIERNWNGMXLFLWTNDNYYLAHTICIIYAFFIYRGPKIMEKRKPFKLEKPLKYW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 QYWTILFQXYW-----YHSITISVLYFILIKVIQKFMENRKPFTLKYPLILW
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                  STRAIN=IOWA;
Millership J.J., Zhu G.;
"Putative long-chain fatty-acyl elongase gene from Cryptosporidium
                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 323;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
25.7%; Score 396.5; DB 5; Length 3;
Best Local Similarity 36.4%; Pred. No. 4.8e-27;
Matches 100; Conservative 35; Mismatches 101; Indels
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Blanchard M., Bradshaw H.;
"The sequence of C. elegans cosmid F41H10.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIM=Bristol N2;
STRAIM=Bristol N2;
SUBMITTED (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                        Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           EMEL; AY204875; AA034582.1; -. GO; GO:0016021; C:integral to membrane; IEA. InterPro; IPR002076; GNS1_SUR4.
Pfam: PF01151; ELO; 1. SPRGSTIE; ELO; 1. SEGUIENCE 323 AA; 38325 MW; 8AF64F586F9B1EDU CRC64;
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Last annotation update}
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    Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
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MEDLINE=99069613; PubMed=9851916;
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                                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=5664;
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33.5%; Pred. No. 1.5e-24;
tive 52; Mismatches 103; Indels 12;
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
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Genome Res 8:135-145(1998).

Genome Res 8:135-145(1998).

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301 AA; 34215 MW; P610D0DA156B1549 CRC64;
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235 PCLLMBISYVVLFGNFYYQSYIKGGGKKFNAEK 267
                                                                                                                                                                                                                                                                                                                                              301 AA
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(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
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Matches 84; Conservative
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PROSITE; PS01188; EL
SEQUENCE 301 AA:
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MEDLINE=99069613; PubMed=9851916;
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Q203100 (CTEMBLE) 01, C.
01-NOV-1996 (TEMBLE) 01, L.
01-NOV-1996 (TEMBLE) 01, L.
01-NOV-2003 (TEMBLE). 24, L.
F41H10.7 protein.
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nes 77; Conservative 4
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Science 282:2012-2018(1998)
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                                                     280 KAV 282
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                        286 KSV
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Q2030
ID Q2030
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DT 01-NO
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                                                LRSLYAEGFYKTLCYSCNPTDVA-----AFWSPAFALSKIVELGDTMPIILRKRPLIFL 161
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28 FDDYFDVLVYSEVLYVLIVPLGPKAMESREPYRLRYLIAAWNLALSFLSLCGTIGVSIML 87
                                                                        40 FADHFDVTIQASILYMVVVEGTKWEMRNRQPFQLTIPINIWNFILAAFSIAGAVKMTPEF
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Rhabditidae, Peloderinae, Caenorhabditis.
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31.3%; Pred. No. 7.2e-24;
ive 58; Mismatches 107; Indels
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chain POLYUNSATURATED fatty acid elongation enzyme.
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2000) to the BMBL/GenBank/DDBJ databases
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SEQUENCE 288 AA; 33561 MW; 8BASCD4892012B0E CRC64;
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G0; G0.001601; C:integral to m
InterPro; IPR002076; GNS1_SUR4.
Pfam; PF01151; ELO; 1.
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01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
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CEELO1 OR F56H11.
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203 IVSANGYRLPKNVSNTVTTVQTTQMLAGV-GITWAVYKVKT-SYKLPCQQSVANLYLAFV 260
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                 Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Indels
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Last annotation update)
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Last annotation update)
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31.7%; Pred. No. 3.9e-21;
ive 49; Mismatches 93;
281 AA.
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Caenorhabditis elegans

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55 SITISVLYFILLIKVIQKEMENRKPFTLKYPLILMNGALAAFSIIATLRFSIDPLRS-LYA 113
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      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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21.2%; Score 327.5; DB 5; Length 286;
Best Local Similarity 32.8%; Pred. No. 5.4e-21;
Matches 80; Conservative 44; Mismatches 109; Indels 11;
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| SEQUENCE FROM N.A.
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| STAAIN=Eristol N2;
| Waterston R.;
| Waterston R.;
| Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
| EMBL; UG1954; AAK29808.1;
| R SEQUENCE FAIHIO.7; CE10284.
| WormPep; F41HIO.7; CE10284.
| R GO; GO:0016021; C:integral to membrane; IEA.
| R GO; GO:0010076; GINSI_SUR4.
| R Ffam; PF01151; ELO; 1.3102 MW; CS0E1180DCB10AC3 CRC64;
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans cosmid F41H10.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
STRALINEBYISCOL NZ;
MEDLINE=99069613; PubMed=9851916;
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274 AKDQ 277
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Search completed: June 16, 2004, 15:29:00 Job time: 47 secs

Sequence Seguence 88, Appl 86, Appl 87, Appl 45, Appl 45, Appl 27, Appl 16, Appl 16, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 11, Appl 12, Appl 12, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18,

Sequence Seq

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63 PRFQLRGPLIIMNTLLAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCGFWT 122
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(al Similarity 37.7%) Pred. No. 3.3e-44;
103; Conservative 54; Mismatches 99; Indels 17
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| OTHER INFORMATION: Xaa = Unknown or Other at position 235
| US-09-903-456-58
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GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Hennard, Fundip
APPLICANT: Hennard, Amanda Bun-Yeong
APPLICANT: Hennard, Yung-Sheng
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APPLICANT: Hennard, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: BEFRENCE: 6407.US.PS
FILE REFRENCE: 6407.US.PS
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOGTWARR: FESTER FOR Windows Version 4.0
US-09-903-456-78
US-09-903-456-80
US-09-903-456-79
US-09-903-456-66
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US-09-903-456-61
US-09-145-828-16
US-09-903-456-85
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; Sequence 58, Application US/09903456
; Patent No. 6677145
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ORGANISM: Drosophila melanogaster
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         NAME/KBY: VARIANT
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; OTHER INFORMATION: Xaa = Unknown or Other at position 272
US-09-903-456-24
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NAME/KEY: VARIANT
LOCATION: (272)...(272)
OTHER INFORMATION: Xaa = Unknown or other at position 272
US-09-145-828A-18
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GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Mukerji, Pradip
APPLICANT: Heonard, Amanda Eun-Yeong
APPLICANT: Beang, Yung-Sheng
APPLICANT: Perceira, Suzette L.
TITLE OF INVENTION: BLONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT FAPLICATION NUMBER: US/09/903,456
CURRENT FALING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 24
LENGTH: 272
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FILE REFERENCE: 6407.US.O1
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
SUMMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Murine
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LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 HSVMYSYYALKAARFNPPRFISMIITSLQLAQMIIGCAINVWANGFLKTHGTXSCHISQR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 EBYWVSFLIVVVYLLLIVVGQTYMRTRKSFSLQRPLILMSFFLAIFSILGTLRMWKFMA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 271;
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                                                                                                                                                                                                                                                                                                                                                 us-uy-yu3-456-53

Sequence 53, Application US/09903456

Patent No. 6677140:
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mikerij, Pradip
APPLICANT: Hearij, Pradip
APPLICANT: Hearij, Vung-Sheng
APPLICANT: Hearij, Vung-Sheng
APPLICANT: Recreira, Surette L.
TILLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
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APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Thurng, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen Jerkehen APPLICANT: Kirchner, Stephen Jerker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 4;
1.6e-43;
                                                                                                                                                                 243 NINLSIAMYSSYFVLFARFFYKAYLAPGGHKSR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch
al Similarity 41.6%; Pred. No. 1
101; Conservative 47; Mismatch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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US-09-903-456-53
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Best Local S
Matches 101
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Indels
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Lang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPRENCE: 607. US. P3
CURRENT RILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 1099-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1998-09-02
NUMBER: OF SEQ ID NOS: 116
SOFTWARE: FaetSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Manada Eun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Perairs, Suzette L.
TILLE OF INVANTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 435.5; DB 4;
35.8%; Pred. No. 7.5e-39;
tive 54; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 VTFAILFIQFFVKAYIIKSSKKSKS 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 55, Application US/09903456; Patent No. 6677145; GENERAL INFORMATION:
                                                                                                                                                                       S-09-903-456-64
Sequence 64, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
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Best Local Similarity 35.8'
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
                                                            281 SSKKSK 286
                                                                                                253 GGHKSR 258
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US-09-903-456-55
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                                                                                                                                       AVLIYTVHSGAEHTAAGRPYILMNYPAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQM 227
                                                                                                                                                                                                                                     49 QKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDPL 108
                                                                                                                                                                                                                                                                                        228 LAGV--GITWMVYKVKTEYKLPCQQSVANEYLAFVIYVTFAILFIQFFVKAYIIKSSK-K 284
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                                                                                    32 EEYWVSSFLIVVVYLLLIVVQQTYMRTRKSFSLQRPLILMSFFLAIFSILGTLRWWKFMA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 WIWVF---YYCGI----YMLVIFGGQHFMQNRPRPQLRGPLIIWNTLLAMFSIMGAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 WILLFOKYWYHSITISVLYFILIKVIOKFMENRKPFTLKYPLILWNGALAAFSIIATLRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%; Score 476.5; DB 4; Length 261; 40.2%; Pred. No. 2.8e-43; tive 49; Mismatches 87; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (218)...(218)
OTHER INFORMATION: Xaa = Unknown or Other at position 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories
APPLICANT: Mikerji, Pradip
APPLICANT: Mikerji, Pradip
APPLICANT: Hoang, Yung-Sheng
APPLICANT: Heang, Yung-Sheng
APPLICANT: Heang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
ITILB OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPRENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 2000-07-24
PRIOR PILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 116
        41.6%; Pred. No. 1.6e-43; ative 47; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60, Application US/09903456 Patent No. 6677145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 40.23
Matches 99; Conservative
      Local Similarity 41.6
nes 101; Conservative
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86 ILWNGALAAPSIIATLRFSIDPLRSLYAEGFYKTLC---YSCNPTDVAAFWSFAFALSKI 142
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                                                                                                                                                                                                                                                                                                                                                       203 TVSAMGYRLPKWVSMTVTTVQTTQMLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIY 262
                                                                                                                              63
                                                                                                                10 EYBFEKQFNENBAIQ---W---MQENWKKSFLFSALYAAFIFGGRHLMUKRAKPELRKPL
                                                                                                                                                                                                                                                                                            26 KYKYSYHFPGEQVADPQYWTILFQKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPL
DB 4; Length 265;
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167 AAVLIYTVHSGAEHTAAGRFYILMAYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
                                                                                                                                                                                                                      227 MLAGVGITWMVYKVKTBYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSK-KS 285
                                                                                                                                                                                                                                                                                                                 77 FGIIANKGIVASYCKVPDFTKGENGYWVWLFWASKLFELVDTIFLVLRKRFLMFLMYHH 136
                                                                                                                                                                                          167 AAVLIYTVHSGAEHTAAGRFYILMNYFAHSLMYTYYTVSAMGYRLPKWVSMTVTTVQTTQ 226
48 FOKYWYHSITISVLYFILIKVIQKFMENRKPFTLKYPLILWNGALAAFSIIATLRFSIDP 107
                           17 FADHEDVILGASILYMVVVGTKWFMRNRQPPQLTIPLNIWNFILAAFSIAGAVKMTPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 FADHFDVILQASILYMVVVFGTKWFWRNRQPPQLTIPLNIWNFILAAFSIAGAVKWTPBF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 MLAGVGITWMVYKVKTEYKLPCQQSVANLYLAFVIYVTFAILFIQFFVKAYIIKSSK-KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 LRSLYAEGFYKTLCYSCNPT-DVAAFWSFAFALSKIVELGDTMFIILRKRPLIFLHYYHH
                                                                                                108 LRSLYAEGFYKTLCYSCNPT-DVAAFWSFAFALSKIVELGDTMPIILRKRPLIFTLHYYHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mukerij, Pradip

APPLICANT: Honard, Amanda Bun-Yeong

APPLICANT: Heonard, Amanda Bun-Yeong

APPLICANT: Heonard, Suzette L.

ITTLE OF INVENTION: BLONGASE GENES AND USES THEREOF

FILE REPERENCE: 460.108. P3

CURRENT APPLICATION NUMBER: US/09/903,456

CURRENT FILING DATE: 2001-07-11

PRIOR APPLICATION NUMBER: US 09/624,670

PRIOR PILING DATE: 2000-07-24

PRIOR PILING DATE: 1999-08-23

PRIOR PILING DATE: 1999-08-02

PRIOR APPLICATION NUMBER: US 09/145,828

PRIOR APPLICATION NUMBER: US 09/145,828

PRIOR APPLICATION NUMBER: US 09/145,828

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PRIOR APPLICATION NUMBER: US 09/145,828
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US-09-903-456-56
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257 KAV 259
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llarity 31.3%; Pred. No. 1e-30;
Conservative 58; Mismatches 107; Indels
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Best Local Similarity 31.3%; Pred. No. 1e-30;
Matches 76; Conservative 58; Mismatches 107; Indels
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Laboratories
APPLICANT: Lenard, Bun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette I.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REPERENCE: 607.08.29
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PILING DATE: 1999-08-23
PRIOR PILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SEQ ID NOS: 116
SEQ ID NO SES
                           CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION WHBER: US 09/624,670
FRIOR FILING DATE: 2000-07-24
PRIOR PLING DATE: 1999-08-23
PRIOR PLING DATE: 1999-08-23
PRIOR PLING DATE: 1999-08-23
PRIOR PLING DATE: 1999-09-02
NUMBER: OF SEQ ID NOS: 116
SEQ ID NOS: 116
SEQ ID NO 55
       CURRENT APPLICATION NUMBER: US/09/903,456
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Patent No. 6677145
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Caenorhabditis elegans
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US-09-903-456-89
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Matches 76; Conserv
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US-09-903-456-55
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ORGANISM:
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                                                                                                          APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Bereira, Suzette L.
ITILE OF INVENTION: BLONGASE GENES AND USES THEREOF
FILE REFRENCE: 6407-US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2001-07-11
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
TILLE OF INVENTION: THE BLONGASE GENE AND USE,
TILLE OF INVENTION: THE BLONGASE GENE AND USE,
CURRENT APPLICATION NUMBER: US/09/145, 828A
CURRENT FILING DATE: 1998-09-02
MUNDHER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Wi-'.
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                                           Sequence 62, Application US/09903456 Patent No. 6677145 GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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US-09-145-828A-13
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LENGTH: 288
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                                                                                                          Length 238;
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APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Laborard, Amanda Eun-Yeong
APPLICANT: Huang, Yung-Shang
APPLICANT: Huang, Yung-Shang
APPLICANT: Pereira, Suzette L.
TITLE OF INVERTION: ELLOWGASE GENES AND USES THEREOF
FILE REPRENCE: 6007.US.P3
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR PLING DATE: 1999-08-23
PRIOR PLING DATE: 1999-08-23
PRIOR PLING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOUTHARD: PASSES OF WINDOWS Version 4.0
SEQ ID NO 26
LENGTH: 238
                                                                                                       Query Match 21.2%; Score 327.5; DB 4;
Best Local Similarity 33.9%; Pred. No. 2.8e-27;
Matches 75; Conservative 46; Mismatches 91;
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33.9%; Pred. No. 2.8e-27;
tive 46; Mismatches 91
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TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Caenorhabditis elegans
US-09-903-456-20
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Best Local Similarity 33.9'
Matches 75; Conservative
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US-09-903-456-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
21.2%; Score 327.5; DB 4; Length 278;
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels 11;
                                                                                                                                                   APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Rirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT PILIG DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 18, Application US/09903456
Patent No. 6677145
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: ELDOGASE GENES AND USES THEREOF
FILE REPRENCE: 6407.US. P3
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR APPLICATION NUMBER: US 09/426,070
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 116
                 Sequence 11, Application US/09145828A
Patent No. 6403349
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11
                                                                                     APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda B. Y.
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US-09-145-828A-11
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US-09-903-456-18
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LENGTH: 278
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89 DGFSHTYSHVSELYIDSTSGYMIFLWVISKIPELDIVFIVLRKRPLIFMEMYHHALIGY 148
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                                                                                                                                                                           Query Match
21.2%; Score 327.5; DB 4; Length 2
Best Local Similarity 32.8%; Pred. No. 3.5e-27;
Matches 80; Conservative 44; Mismatches 109; Indels
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LOCATION: (141)...(141)
OTHER INFORMATION: Xaa = Unknown or Other at position 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abbott Laboratories APPLICANT: Mikerji, Pradip APPLICANT: Mikerji, Pradip APPLICANT: Mikerji, Pradip APPLICANT: Huang, Yung-Sheng APPLICANT: Huang, Yung-Sheng APPLICANT: Huang, Yung-Sheng APPLICANT: Presira, Suzatte L. TITLE OF INVEXTION: ELONGASE GENES AND USES THEREOF FILE REFERENCE: 6407.US.P3.

CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR PLILNG DATE: 2000-07-24
PRIOR PLILNG DATE: 1999-08-23
PRIOR PLILNG DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR PLILNG DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-903-456-47
; Sequence 47, Application US/09903456
; Patent No. 6677145
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18
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ORGANISM: Homo sapiens
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61 AGFRVSRKFAMFITLSQITQMLMGCVVNYLVFCWMQHDQ--CHSHFQNIFWSSLMYLSYL 118

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267 ILFIQFPVKAYIIKSSKKSKS 287 :|| || :|| || :|| 119 VLFCHPFFFAYIGKMRKTTKA 139

Search completed: June 16, 2004, 15:30:08 Job time: 24 secs